

GenCore version 5.1.3  
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 OM protein - protein search, using sw model  
 Run on: October 9, 2002, 19:12:30 ; Search time 12.1071 Seconds  
 (without alignments)  
 1036.689 Million cell updates/sec

Title: US-09-822-698A-1  
 Perfect score: 113  
 Sequence: 1 EIVLTOSPLSLPVTGEPAS.....MQLQSFTEGPTGKVDIKR 113  
 Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0  
 Searched: 747574 seqs, 111073796 residues  
 Word size : 0  
 Total number of hits satisfying chosen parameters: 747574  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Listing first 45 summaries

Database : A.Geneseq\_032802.\*  
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 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	113	100.0	113	22	AAEL2705	Human PH1 Fab anti
2	113	100.0	220	22	AAEL2714	Human recombinant
3	113	100.0	381	22	AAEL2707	Human bivPH1-IL-2
4	32	28.3	222	22	AAU04972	Synthetic antibody
5	32	28.3	222	22	AAU04976	Synthetic antibody
6	31	27.4	100	16	AAU04976	VK005 VK region.
7	31	27.4	100	22	AAEL2711	Antibody variable
8	31	27.4	111	21	AAV95225	Anti-platelet glyco
9	31	27.4	112	17	AAV95218	Human IgM GM607 va
10	31	27.4	113	21	AAV95220	Anti-platelet glyco
11	31	27.4	113	21	AAV95221	Anti-platelet glyco

12	31	27.4	114	18	AAW27544	Human Ab light cha
13	31	27.4	114	21	AAV95186	Anti-platelet glyco
14	31	27.4	131	21	AAV95226	Anti-platelet glyco
15	31	27.4	139	22	AAAB99117	Human protein seq
16	31	27.4	157	22	AAW77307	Human bone marrow
17	31	27.4	248	22	AAAG5590	Anti-hEDRF antibod
18	31	27.4	281	18	AAW27560	Consensus single c
19	30	26.5	239	21	AAV82613	Human pThrp monocl
20	30	26.5	239	21	AAV82615	Human pThrp monocl
21	29	25.7	112	22	AAAG93587	Human anti-Rh(D) c
22	28	24.8	239	21	AAV82616	Human pThrp monocl
23	27	23.9	109	20	AAV39809	TRI 6 antibody lig
24	27	23.9	112	19	AAW53586	Light chain of a h
25	27	23.9	148	20	AAV34309	IgM antibody CEM 1
26	27	23.9	239	21	AAV82612	Human pThrp monocl
27	27	23.9	239	21	AAV82614	Human pThrp monocl
28	27	23.9	239	21	AAV82617	Human pThrp monocl
29	26	23.0	100	16	AAV72067	OF7K.7 VK-2 L cha
30	26	23.0	100	22	AAE06968	Mouse germline kap
31	26	23.0	108	14	AAV83594	Human lambda light
32	26	23.0	108	19	AAW58494	Human kappa light
33	25	22.1	112	19	AAW54015	Human anti-CD4 ant
34	25	22.1	116	19	AAW76126	Human ICR-8.1 V-K
35	25	22.1	116	19	AAW71256	Humanised murine a
36	25	22.1	116	20	AAW81450	Humanised antibody
37	25	22.1	116	21	AAAB13046	Protein sequence o
38	25	22.1	116	21	AAV82445	Humanised ICR-8.1
39	25	22.1	116	21	AAV50753	Humanised murine a
40	25	22.1	138	19	AAV53812	Light chain of a h
41	25	22.1	222	22	AAU04974	Synthetic antibody
42	24	21.2	112	14	AAV32239	Humanised MAB high
43	24	21.2	112	18	AAV27145	Mature light chain
44	24	21.2	112	21	AAV87571	Humanised ABL 364
45	24	21.2	143	20	AAV34313	IgM antibody CEM 1

# ALIGNMENTS

RESULT 1  
 AAEL2705  
 ID AAEL2705 standard; Protein; 113 AA.  
 XX AC AAEL2705;  
 XX DT 04-JAN-2002 (first entry)  
 XX DE Human PH1 Fab antibody variable light chain region (VL).  
 XX KW Human: tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;  
 KW variable light chain region; cancer; breast; ovary; lung; bladder;  
 KW cytosolic; therapy; PH1 antibody.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT Region 24..39  
 FT /label= CDR1  
 FT /note= "Complementarity determining region 1"  
 FT Region 55..61  
 FT /label= CDR2  
 FT /note= "Complementarity determining region 2"  
 FT Region 94..102  
 FT /label= CDR3  
 FT /note= "Complementarity determining region 3"  
 WO200175110-A2.  
 PD 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US10589.  
 XX 30-MAR-2000; 2000US-0538913.  
 PR

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XX PA (DYAX-) DYAX CORP.
XX PI Hoogenboom HRJM, Henderikx MPG;
XX DR WPI: 2001-626437/72.
XX DR N-PSDB; AAD20730.
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1
XX PS Claim 3; Page 93; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC detection method selected from enzyme-linked immunosorbent assay,
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
XX CC antibody VL region.
XX SQ Sequence 113 AA;
Query Match 100.0%; Score 113; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTGEPASTSCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVLPVTGEPASTSCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
QY 61 SGVPDRFGSGVSGDTFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFGSGVSGDTFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 113
RESULT 2
AAE12714
ID AAE12714 standard; Protein; 220 AA.
AC AAE12714;
XX 04-JAN-2002 (first entry)
XX Human recombinant immunoglobulin (Ig) light chain region.
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
XX light chain region; cancer; breast; ovary; lung; bladder;
XX cytostatic; therapy; immunoglobulin; Ig.
XX Homo sapiens.
XX WO200175110-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10589.
XX 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX
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XX

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PI Hoogenboom HRJM, Henderikx MPG;
XX WPI: 2001-626437/72.
XX DR N-PSDB; AAD20744.
XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1
XX PS Claim 12; Page 103; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC detection method selected from enzyme-linked immunosorbent assay,
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human recombinant immunoglobulin
XX CC (Ig) light chain region (variable VL and CL constant kappa light chain).
XX SQ Sequence 220 AA;
Query Match 100.0%; Score 113; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.2e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTGEPASTSCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVLPVTGEPASTSCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
QY 61 SGVPDRFGSGVSGDTFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFGSGVSGDTFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 113
RESULT 3
AAE12707
ID AAE12707 standard; Protein; 381 AA.
AC AAE12707;
XX 04-JAN-2002 (first entry)
XX Human b1vPH1-IL-2 immunocytokine protein.
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX Homo sapiens.
XX WO200175110-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10589.
XX 30-MAR-2000; 2000US-0538913.
XX (DYAX-) DYAX CORP.
XX Hoogenboom HRJM, Henderikx MPG;
XX WPI: 2001-626437/72.
XX DR N-PSDB; AAD20732.
XX

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DT 24-OCT-2001 (first entry)

XX Synthetic antibody scFv UBS-54, mutant B43.

DE Human; Antibody; scFv UBS-54; VH1; VK2; phage display; B43;

KW tumour; tissue penetration; complement activation; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key

FH Location/Qualifiers

FT 1..25

FT /label= FR1

FT 26..32

FT /label= CDR1

FT /note= "Complementarity determining region"

FT 33..51

FT /label= FR2

FT 52..57

FT /label= CDR2

FT /note= "Complementarity determining region"

FT 58..98

FT /label= FR3

FT 99..104

FT /label= CDR3

FT /note= "Complementarity determining region"

FT 105..112

FT /label= FR4

FT 113..135

FT /label= FR1

FT 136..151

FT /label= CDR1

FT /note= "Complementarity determining region"

FT 152..166

FT /label= FR1

FT 167..173

FT /label= CDR1

FT /note= "Complementarity determining region"

FT 174..205

FT /label= FR4

FT 206..214

FT /label= CDR1

FT /note= "Complementarity determining region"

FT 215..222

FT /label= FR1

XX WO200148485-A2.

XX 05-JUL-2001.

XX 21-DEC-2000; 2000WO-NL00941.

XX 27-DEC-1999; 99EP-0204561.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Logtenberg T;

XX WPI; 2001-441741/47.

XX Use of a native group for selecting evolved binding members with

PT enhanced group binding, complement activation and tissue penetration

PT property from library of mutants of a protein capable of binding to the

PT group -

XX Example; Page - ; 42pp; English.

XX The sequence represents the synthetic antibody scFv UBS-54, mutant B43,

CC where VK2 forms the light chain (VH1 forming the heavy chain). The

CC antibody molecule is used to demonstrate the method of the invention

CC which involves using a cell displaying a group (e.g. a phage displayed

CC antibody) to isolate an evolved (or mutated) molecule which has a

CC higher affinity/enhanced property for the group. The method is useful for

CC obtaining an evolved group binding molecule with enhanced group binding,

CC tissue penetration or complement activation property. The selection

CC procedure is useful for selecting high affinity mutant antibody fragments

CC which are useful for targeted tumour cell lysis. Mutants of proteinaceous

CC molecule are physically linked to a vehicle comprising nucleic acid

CC encoding the mutant molecule and this has the advantage that when the

CC member is recovered from the cells and/or its functional equivalent, the

CC nucleic acid encoding the proteinaceous molecule can also be

CC simultaneously recovered.

CC Note: The present sequence is not displayed in the specification

CC but is derived from the scFv UBS-54 sequence given in figure 2.

XX SQ Sequence 222 AA;

Query Match 28.3%; Score 32; DB 22; Length 222;

Best Local Similarity 100.0%; Pred. No. 3.3e-23;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTQSPFLSLPVTGPSPASISCRSSQSLHSHNGY 35

DB 116 LTQSPFLSLPVTGPSPASISCRSSQSLHSHNGY 147

|||||

RESULT 6

AAR72066

ID AAR72066 standard; Protein; 100 AA.

XX AC AAR72066;

DT 26-SEP-1995 (first entry)

XX VK005 VK region.

DE

XX

KW Graves ophthalmopathy associated immunoglobulin protein;

KW orbital antigen; monoclonal antibody; light chain; L chain;

KW variable region; autoimmunity.

XX OS Homo sapiens.

XX FH Key

FT Region

FT 23..38

FT /label= CDR1

FT 54..60

FT /label= CDR2

FT 93..100

FT /label= CDR3

XX WO9508336-A.

XX 30-MAR-1995.

XX 22-SEP-1994; 94WO-US10756.

XX 22-SEP-1993; 93US-0124469.

XX (NICH-) NICHOLS INST DIAGNOSTICS.

XX McIachlan SM, Rapoport B;

XX WPI; 1995-139383/18.

XX N-PSDB; AAQ89325.

XX Graves' ophthalmopathy-associated monoclonal antibody - produced

PT by molecular cloning of immunoglobulin genes by PCR

XX Disclosure; Page 67; 94pp; English.

XX L- and H-chain DNA was amplified by PCR from Graves' orbital

CC tissue and clones encoding autoimmune-associated immunoglobulin

CC fragments were obtained. 14/15 clones of L chain (kappa) regions

CC showed homology to the putative VK germline gene KL012 (given in

CC AAQ89317) and the remaining clone, OF7K.7 (AAQ89326), to the VK005

CC gene.





CC diseased arteries, bypass grafts, dialysis etc., and can also be  
 CC used as diagnostic reagents. Methods of inhibiting aggregation  
 CC of platelets, of binding human platelet GPIb alpha and of selecting  
 CC a VH or VL region of an antibody that inhibits platelet aggregation  
 CC are claimed.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the HIB-5 VH sequence given in Fig 8 (see AAY95220).  
 XX  
 SQ Sequence 111 AA;

Query Match 27.4%; Score 31; DB 21; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPAISCRSSQSLHLSNGY 35  
 |||||  
 Db 5 TQSPSLPVTGPGEPAISCRSSQSLHLSNGY 35

RESULT 9  
 AAR95218  
 ID AAR95218 standard; protein; 112 AA.

XX AAR95218;

DT 16-DEC-1996 (first entry)

XX Human IgM GM607 variable light chain.

DE Antibody: fusion protein; single chain; inhibition; tumour;  
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;  
 KW immunoassay; Lewis(Y) carbohydrate antigen.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Domain 24..39  
 FT /label= CDR 1.  
 FT Domain 55..61  
 FT /label= CDR 2.  
 FT Domain 89..97  
 FT /label= CDR 3.

XX W09613594-A1.

XX 09-MAY-1996.

XX 26-OCT-1995; 95WO-US13811.

XX 28-OCT-1994; 94US-0331398.

XX 28-OCT-1994; 94US-0331396.

XX 28-OCT-1994; 94US-0331397.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;

XX Padlan EA, Pai L, Pastan I, Willingham M;

XX WPI; 1996-251462/25.

XX Single chain fusion proteins and antibodies - useful to diagnose and

XX treat cancer, specifically bind Lewis(Y) related carbohydrate

XX antigen

XX Example 13; Figure 11B; 116pp; English.

XX A novel recombinant DNA molecule which encodes a single chain fusion  
 CC protein or antibody comprising the Fv region of both the light and  
 CC heavy chains of an antibody (Ab) fused together, and an effector  
 CC molecule, where the fusion protein or Ab has the binding specificity  
 CC of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production  
 CC -of such fusion proteins or antibodies. The fusion proteins can be  
 CC used in compositions as an immunotoxin to inhibit tumour cell growth.

CC The single chain antibody can be used to detect the presence or  
 CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a  
 CC patient. The antibodies are also useful as multiple targeting  
 CC moieties, providing at least 2 kinds of biological activity. They  
 CC can also be used in diagnostic assays and for the imaging of tumours  
 CC when attached to a radiolabel and for the pathological diagnosis of  
 CC tumours. Humanised antibodies are less immunogenic than the mouse  
 CC MAbs B1, B3 and B5, making them more suitable for long term  
 CC treatment.

XX SQ Sequence 112 AA;

Query Match 27.4%; Score 31; DB 17; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPAISCRSSQSLHLSNGY 35  
 |||||  
 Db 5 TQSPSLPVTGPGEPAISCRSSQSLHLSNGY 35

RESULT 10  
 AAY95220

ID AAY95220 standard; protein; 113 AA.

XX AAY95220;

XX 29-AUG-2000 (first entry)

DE Anti-platelet glycoprotein Ib human HIB-5 VL.

XX Variable light chain; single chain antibody; scFv; human; HIB-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Region 1..23  
 FT /note= "framework region 1"  
 FT Region 24..39  
 FT /note= "complementarity determining region 1"  
 FT Region 40..54  
 FT /note= "framework region 2"  
 FT Region 55..61  
 FT /note= "complementarity determining region 2"  
 FT Region 62..93  
 FT /note= "framework region 3"  
 FT Region 94..101  
 FT /note= "complementarity determining region 3"  
 FT Region 102..113  
 FT /note= "framework region 4"

XX W0200026667-A1.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US25495.

XX 30-OCT-1998; 98US-0106275.

XX (MILL) MILLER J L.

XX Miller JL;

XX WPI; 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet  
 CC glycoprotein Ib alpha molecule useful for producing antibodies which  
 CC inhibit platelet aggregation -  
 XX Claim 18; Fig 8; 89pp; English.

CC The present sequence is that of the light chain variable region  
 CC (VL) of human single chain antibody (scFv) H1b-5, which is directed  
 CC against platelet glycoprotein Ib (GPIb). The H1b series of scFv  
 CC was isolated from a human synthetic VH and VL scFv library by 3  
 CC rounds of phagemid selection against transfected CHO cells  
 CC expressing the GPIb alpha component of the GPIb/IX/V complex  
 CC on their surface, followed by a 4th round of selection against  
 CC washed human platelets, and 2 final rounds in which attempts were  
 CC made to displace scFv from washed platelets by flooding with  
 CC murine monoclonal antibody or mimotope peptide (see AA95229).  
 CC whether displayed as surface proteins on a phagemid or secreted  
 CC as free scFv by Escherichia coli, the H1b scFv clones are capable  
 CC of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences  
 CC and are therefore attractive potential reagents for therapeutic  
 CC purposes. They provide a new class of antithrombotic agents,  
 CC useful for the prevention of platelet-dependent thrombi in  
 CC diseased arteries, bypass grafts, dialysis etc., and can also be  
 CC used as diagnostic reagents. Methods of inhibiting aggregation  
 CC of platelets, of binding human platelet GPIb alpha and of selecting  
 CC a VH or VL region of an antibody that inhibits platelet aggregation  
 CC are claimed.

XX SQ Sequence 113 AA;

Query Match 27.4%; Score 31; DB 21; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22; Indels 0; Gaps 0;  
 Matches 31; Conservative 0; Mismatches 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35  
 DB 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

RESULT 11

AA95221  
 ID AA95221 standard; Protein; 113 AA.

XX AC AA95221;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human H1b-5 VL.

XX KW Variable light chain; single chain antibody; scFv; human; H1b-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..23 /note= "framework region 1"  
 FT Region 24..39 /note= "framework region 1"  
 FT Region 40..54 /note= "framework region 2"  
 FT Region 55..61 /note= "framework region 2"  
 FT Region 62..93 /note= "framework region 3"  
 FT Region 94..101 /note= "framework region 3"  
 FT Region 102..113 /note= "framework region 3"  
 FT Region /note= "framework region 4"

XX PN WO200026667-A1.

XX XX 11-MAY-2000.

XX XX 29-OCT-1999; 99WO-US25495.

XX XX 30-OCT-1998; 98US-0106275.

XX (MILLER) MILLER J L.  
 XX PA  
 XX PI Miller JL;  
 XX WI; 2000-365744/31.  
 XX DR  
 XX PT Isolated nucleic acid molecule encoding anti-human platelet  
 PT glycoprotein Ib alpha molecule useful for producing antibodies which  
 PT inhibit platelet aggregation -  
 XX PS  
 XX Claim 18; Fig 8; 89pp; English.

XX The present sequence is that of the light chain variable region  
 CC (VL) of human single chain antibody (scFv) H1b-5, which is directed  
 CC against platelet glycoprotein Ib (GPIb). The H1b series of scFv  
 CC was isolated from a human synthetic VH and VL scFv library by 3  
 CC rounds of phagemid selection against transfected CHO cells  
 CC expressing the GPIb alpha component of the GPIb/IX/V complex  
 CC on their surface, followed by a 4th round of selection against  
 CC washed human platelets, and 2 final rounds in which attempts were  
 CC made to displace scFv from washed platelets by flooding with  
 CC murine monoclonal antibody or mimotope peptide (see AA95229).  
 CC whether displayed as surface proteins on a phagemid or secreted  
 CC as free scFv by Escherichia coli, the H1b scFv clones are capable  
 CC of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences  
 CC and are therefore attractive potential reagents for therapeutic  
 CC purposes. They provide a new class of antithrombotic agents,  
 CC useful for the prevention of platelet-dependent thrombi in  
 CC diseased arteries, bypass grafts, dialysis etc., and can also be  
 CC used as diagnostic reagents. Methods of inhibiting aggregation  
 CC of platelets, of binding human platelet GPIb alpha and of selecting  
 CC a VH or VL region of an antibody that inhibits platelet aggregation  
 CC are claimed.

CC Note: The present sequence is not shown in the specification but is  
 CC derived from the H1b-5 VH sequence given in Fig 8 (see AA95220).

XX SQ Sequence 113 AA;

Query Match 27.4%; Score 31; DB 21; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-22; Indels 0; Gaps 0;  
 Matches 31; Conservative 0; Mismatches 0;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human H1b-5 VL.

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

DB 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

RESULT 12

AAW27544  
 ID AAW27544 standard; Protein; 114 AA.

XX AC AAW27544;

XX DT 22-JAN-1998 (first entry)

XX DE Human Ab light chain variable region V-kappa-2 consensus.

XX KW Human; antibody; preparation; library; V-kappa-2; variable region;  
 KW light chain; consensus.

XX OS Homo sapiens.

XX PN WO9708320-A1.

XX XX 06-MAR-1997.

XX XX 19-AUG-1996; 96WO-EP03647.

XX XX 18-AUG-1995; 95EP-0113021.

XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;  
 XX WPI; 1997-179277/16.  
 DR N-PSDB; AAY87942.  
 XX  
 XX Preparation of human derived antibody gene library - using synthetic  
 PT consensus sequences, and signal consensus antibody gene as universal  
 PT framework for highly diverse antibody libraries  
 XX  
 XX Example 1; Fig 3B; 436pp; English.  
 XX  
 CC The present sequence is the human antibody light chain  
 CC variable region synthetic kappa sequence V-kappa-2, used in the  
 CC preparation of a human derived antibody gene library.  
 XX  
 SQ Sequence 114 AA;  
 Query Match 27.4%; Score 31; DB 18; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 TQSPSLPVTGPSPASISCRSSQSLHSHNGY 35  
 Db 5 TQSPSLPVTGPSPASISCRSSQSLHSHNGY 35  
 RESULT 13  
 AAY95186  
 ID AAY95186 standard; Protein; 114 AA.  
 XX  
 AC AAY95186;  
 XX  
 XX 29-AUG-2000 (first entry)  
 DT  
 XX  
 DE Anti-platelet glycoprotein Ib human Hib-5 VL.  
 XX  
 KW Variable light chain; single chain antibody; scFv; human; Hib-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..23 /note= "framework region 1"  
 FT Region 24..39 /note= "complementarity determining region 1"  
 FT Region 40..54 /note= "framework region 2"  
 FT Region 55..61 /note= "complementarity determining region 2"  
 FT Region 62..93 /note= "framework region 3"  
 FT Region 94..101 /note= "complementarity determining region 3"  
 FT Region 102..114 /note= "framework region 4"  
 XX  
 XX WO200026667-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 XX 29-OCT-1999; 99WO-US25495.  
 XX  
 XX 30-OCT-1998; 98US-0106275.  
 XX  
 XX (MILLER) MILLER J L.  
 XX  
 XX Miller JL;  
 PI  
 XX WPI; 2000-365744/31.  
 DR N-PSDB; AAA27664.

XX Isolated nucleic acid molecule encoding anti-human platelet  
 PT glycoprotein Ib alpha molecule useful for producing antibodies which  
 PT inhibit platelet aggregation -  
 XX  
 PS Claim 11; Page 77; 89pp; English.  
 XX  
 CC The present sequence is that of the light chain variable region  
 CC (VL) of human single chain antibody (scFv) Hib-5, which is directed  
 CC against platelet glycoprotein Ib (GPiB). The Hib series of scFv  
 CC was isolated from a human synthetic VH and VL scFv library by 3  
 CC rounds of phagemid selection against transfected CHO cells  
 CC expressing the GPiB alpha component of the GPiB/IX/V complex  
 CC on their surface, followed by a 4th round of selection against  
 CC washed human platelets, and 2 final rounds in which attempts were  
 CC made to displace scFv from washed platelets by flooding with  
 CC murine monoclonal antibody or mimotope peptide (see AAY95229).  
 CC Whether displayed as surface proteins on a phagemid or secreted  
 CC as free scFv by Escherichia coli, the Hib scFv clones are capable  
 CC of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences  
 CC and are therefore attractive potential reagents for therapeutic  
 CC purposes. They provide a new class of antithrombotic agents,  
 CC useful for the prevention of platelet-dependent thrombi in  
 CC diseased arteries, bypass grafts, dialysis etc., and can also be  
 CC used as diagnostic reagents. Methods of inhibiting aggregation  
 CC of platelets, of binding human platelet GPiB alpha and of selecting  
 CC a VH or VL region of an antibody that inhibits platelet aggregation  
 CC are claimed.  
 XX  
 SQ Sequence 114 AA;  
 Query Match 27.4%; Score 31; DB 21; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 TQSPSLPVTGPSPASISCRSSQSLHSHNGY 35  
 Db 5 TQSPSLPVTGPSPASISCRSSQSLHSHNGY 35  
 RESULT 14  
 AAY95226  
 ID AAY95226 standard; Protein; 131 AA.  
 XX  
 AC AAY95226;  
 XX  
 XX 29-AUG-2000 (first entry)  
 DT  
 XX  
 DE Anti-platelet glycoprotein Ib human Hib-5 VL region and linker.  
 XX  
 KW Variable light chain; single chain antibody; scFv; human; Hib-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.  
 XX  
 OS Chimeric - Synthetic.  
 OS Chimeric - Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..17 /note= "vector-derived linker"  
 FT Region 18..131 /note= "light chain variable region"  
 FT Region 18..40 /note= "framework region 1"  
 FT Region 41..56 /note= "complementarity determining region 1"  
 FT Region 57..71 /note= "framework region 2"  
 FT Region 72..78 /note= "complementarity determining region 2"  
 FT Region 79..110 /note= "framework region 3"

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FT Region 111..119
FT /note="complementarity determining region 3"
FT Region 120..131
FT /note="framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILLER) MILLER J L.
XX Miller JL;
XX WPI; 2000-365744/31.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Disclosure; Fig 8; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) plus linker peptide of human single chain antibody (scFv)
CC H1b-5, which is directed against platelet glycoprotein Ib (GPIb).
CC H1b-5 is composed of a heavy chain variable region and light chain
CC variable region joined via a vector-derived peptide linker. The
CC H1b series of scFv was isolated from a human synthetic VH and VL
CC scFv library by 3 rounds of phagemid selection against transfected
CC CHO cells expressing the GPIb alpha component of the GPIb/IX/V
CC complex on their surface, followed by a 4th round of selection
CC against washed human platelets, and 2 final rounds in which
CC attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or mimotope peptide (see
CC AY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the H1b scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPIb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX
XX Sequence 131 AA;
Query Match 27.4%; Score 31; DB 21; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 TQSPSLPVTPTGEPASICRSQSLLHSNGY 35
Db 22 TQSPSLPVTPTGEPASICRSQSLLHSNGY 52
RESULT 15
AAB99117
ID AAB99117 standard; Protein; 139 AA.
XX
XX AAB99117;
XX
XX 22-AUG-2001 (first entry)
XX Human protein SEQ ID 16.
XX
XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;

```

```

KW signal transduction inhibition; tissue fibrosis; atherosclerosis.
XX Homo sapiens.
XX WO200136642-A1.
XX 25-MAY-2001.
XX 17-NOV-2000; 2000WO-JP08129.
XX 18-NOV-1999; 99JP-0328681.
XX 08-NOV-2000; 2000JP-0340216.
XX (NISHI) JAPAN TOBACCO INC.
XX Sakamoto S, Kamada M;
XX WPI; 2001-343825/36.
XX N-PSDB; AAH41159.
XX Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT useful for treating TGF-beta associated diseases such as tissue
PT fibrosis -
XX Claim 11; Page 109-110; 118pp; Japanese.
XX The present invention relates to novel human monoclonal antibodies. The
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC receptor, resulting in the inhibition of the signal transduction of human
CC TGF-beta into cells. The antibodies can be used for the prevention and
CC treatment of diseases associated with the production of TGF-beta, such as
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC used in the present invention.
XX Sequence 139 AA;
Query Match 27.4%; Score 31; DB 22; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 TQSPSLPVTPTGEPASICRSQSLLHSNGY 35
Db 25 TQSPSLPVTPTGEPASICRSQSLLHSNGY 55
Search completed: October 9, 2002, 19:22:59
Job time : 12.1071 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 4.61224 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 113

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Searched: 231628 segs, 2442594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
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- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	27.4	112	1	US-08-331-398A-49
2	31	27.4	112	2	US-08-331-397B-49
3	31	27.4	112	2	US-08-759-804A-49
4	31	27.4	112	4	US-09-227-693-49
5	31	27.4	113	4	US-09-025-769B-15
6	31	27.4	114	4	US-09-025-769B-29
7	31	27.4	114	4	US-09-025-769B-45
8	31	27.4	281	4	US-09-025-769B-178
9	29	25.7	112	4	US-09-240-374-30
10	28	24.8	112	1	US-08-053-171-16
11	26	23.0	108	1	US-08-488-113B-151
12	26	23.0	108	1	US-08-477-484B-151
13	26	23.0	108	1	US-08-107-669D-15
14	26	23.0	108	1	US-08-472-788A-15
15	26	23.0	108	2	US-08-477-531B-15
16	26	23.0	108	2	US-08-646-360-151
17	26	23.0	108	2	US-08-082-842A-15
18	26	23.0	108	4	US-08-839-765-151
19	26	23.0	108	4	US-09-136-389-151
20	25	22.1	112	1	US-08-478-039-88
21	25	22.1	112	1	US-08-476-349A-88
22	25	22.1	116	1	US-08-482-882-66
23	25	22.1	116	2	US-08-483-389-66
24	25	22.1	116	2	US-08-487-113D-66
25	25	22.1	116	2	US-08-473-503-66
26	25	22.1	116	2	US-08-483-932-66
27	25	22.1	116	2	US-08-720-420A-66

28 25 22.1 116 3 US-08-714-017-66 Sequence 66, Appl  
29 25 22.1 116 3 US-08-475-680-66 Sequence 66, Appl  
30 24 21.2 112 1 US-08-053-171-15 Sequence 15, Appl  
31 24 21.2 112 3 US-08-815-190A-14 Sequence 14, Appl  
32 23 20.4 112 1 US-08-331-398A-50 Sequence 50, Appl  
33 23 20.4 112 2 US-08-331-397B-50 Sequence 50, Appl  
34 23 20.4 112 2 US-08-759-804A-50 Sequence 50, Appl  
35 23 20.4 112 4 US-09-227-693-50 Sequence 50, Appl  
36 23 20.4 113 1 US-08-264-093-10 Sequence 10, Appl  
37 22 19.5 132 1 US-08-392-419-4 Sequence 4, Appl  
38 22 19.5 365 3 US-08-875-811-53 Sequence 53, Appl  
39 22 19.5 366 3 US-08-875-811-55 Sequence 55, Appl  
40 21 18.6 131 1 US-08-129-930B-95 Sequence 95, Appl  
41 21 18.6 131 4 US-08-134-346A-50 Sequence 50, Appl  
42 21 18.6 131 4 US-08-976-288A-95 Sequence 95, Appl  
43 20 17.7 108 1 US-08-468-661-3 Sequence 3, Appl  
44 20 17.7 108 1 US-08-466-272A-3 Sequence 3, Appl  
45 20 17.7 108 1 US-08-478-857-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-331-398A-49  
; Sequence 49, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
; TITLE OF INVENTION: and Their Uses (as amended)  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331,398A  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-126110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

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; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-398A-49

Query Match 27.4%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35

RESULT 2
US-08-331-397B-49
; Sequence 49, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35

RESULT 3
US-08-759-804A-49
; Sequence 49, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA: US 07/767,331
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-759-804A-49

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHLSNGY 35
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-29

Query Match          27.4%; Score 31; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
   |||||
Db 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 7
US-09-025-769B-45
; Sequence 45, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-45

Query Match          27.4%; Score 31; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
   |||||
Db 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 8
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-178

Query Match          27.4%; Score 31; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
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Db 170 TOSPLSLPVTGEPASISCRSSQSLHNSGY 200

RESULT 9
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455

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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      25.7%  Score 29; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  LTQSPSLPVTGPGPASPISCRSSQSLHLS 32
Db   3  LTQSPSLPVTGPGPASPISCRSSQSLHLS 31

RESULT 10
US-08-053-171-16
; Sequence 16, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Sequence of Tew antibody
; Patent No. 5562903

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      25.7%  Score 29; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4  LTQSPSLPVTGPGPASPISCRSSQSLHLS 32
Db   3  LTQSPSLPVTGPGPASPISCRSSQSLHLS 31

RESULT 11
US-08-488-113B-151
; Sequence 151, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
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; TOPOLOGY: linear
US-08-488-113B-151
Query Match 23.0%; Score 26; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSL 30
Db 5 TQSPSLPVTGPEPASISCRSSQSL 30
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RESULT 12
US-08-477-484B-151
; Sequence 151, Application US/08477484B
; Patent No. 5756899
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-477-484B-151
Query Match 23.0%; Score 26; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TOPOLOGY: linear
US-08-472-788A-15
; Sequence 15, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
US-08-472-788A-15
Query Match 23.0%; Score 26; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSL 30
Db 5 TQSPSLPVTGPEPASISCRSSQSL 30
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RESULT 14
US-08-472-788A-15
; Sequence 15, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
US-08-472-788A-15
Query Match 23.0%; Score 26; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSL 30
Db 5 TQSPSLPVTGPEPASISCRSSQSL 30
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RESULT 13
US-08-107-669D-15
; Sequence 15, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbalia
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-15
Query Match 23.0%; Score 26; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.7e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSL 30
Db 5 TQSPSLPVTGPEPASISCRSSQSL 30
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COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,788A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/082,842

FILING DATE: 23-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000003

TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540

TELEX:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-472-788A-15

Query Match 23.0%; Score 26; DB 1; Length 108;

Best Local Similarity 100.0%; Pred. No. 8.7e-18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTPTGEPASISCRSSQSL 30

Db 5 TQSPSLPVTPTGEPASISCRSSQSL 30

#### RESULT 15

US-08-477-531B-15

Sequence 15, Application US/08477531B

Patent No. 5821123

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,531B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Michele A. Cimbala  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-531B-15

Query Match 23.0%; Score 26; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 8.7e-18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TQSPSLPVTPTGEPASISCRSSQSL 30

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Job time : 4.61224 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:10 ; Search time 44.3929 Seconds  
(without alignments)  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	113	100.0	381	19	US-09-538-913-5
5	113	100.0	381	22	US-09-822-698A-5
6	31	27.4	64	26	US-60-173-469-1652
7	31	27.4	80	26	US-60-160-203-4277

8	31	27.4	98	26	US-60-169-840-6274
9	31	27.4	100	5	US-08-124-469-19
10	31	27.4	100	8	US-08-472-771-19
11	31	27.4	100	8	US-08-486-202-19
12	31	27.4	100	18	US-09-430-048-60
13	31	27.4	100	18	US-09-472-087-115
14	31	27.4	100	19	US-09-538-913-19
15	31	27.4	100	22	US-09-822-698A-19
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20	31	27.4	112	7	US-08-331-396C-49
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25	31	27.4	112	11	US-08-759-804-49
26	31	27.4	112	18	US-09-430-048-20
27	31	27.4	113	18	US-09-490-070-15
28	31	27.4	114	18	US-09-430-048-19
29	31	27.4	114	18	US-09-490-070-29
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ALIGNMENTS

RESULT 1  
US-09-538-913-1  
; Sequence 1, Application US/09538913  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Paula  
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE  
; FILE REFERENCE: seglist DYX-15  
; CURRENT APPLICATION NUMBER: US/09/538,913  
; CURRENT FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-538-913-1

Query Match	100.0%	Score 113;	DB 19;	Length 113;
Best Local Similarity	100.0%	Pred. No. 3e-102;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSPSLPVTGPGEASISCRSSQSLLSHNGYTYLDWYLQKPGQSPQLIYSGSHRA	60	
Db	1	EIVLTQSPSLPVTGPGEASISCRSSQSLLSHNGYTYLDWYLQKPGQSPQLIYSGSHRA	60	
QY	61	SGVPDRFSSVSGTDFTLRIKSRVEAEDVGYYCMQGLQSPFTFGPKTKVDIKR	113	
Db	61	SGVPDRFSSVSGTDFTLRIKSRVEAEDVGYYCMQGLQSPFTFGPKTKVDIKR	113	

```
RESULT 2
US-09-822-698A-1
; Sequence 1, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1
Query Match 100.0%; Score 113; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 3
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24
Query Match 100.0%; Score 113; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 5.3e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
```

```
RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPH1-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5
Query Match 100.0%; Score 113; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.4e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPH1-IL-2
US-09-822-698A-5
Query Match 100.0%; Score 113; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.4e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
```

```
RESULT 6
US-60-173-469-1652
```



```
; Sequence 1652, Application US/60173469
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000185
; CURRENT APPLICATION NUMBER: US/60/173,469
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 2120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1652
; LENGTH: 64
; TYPE: PRT
; ORGANISM: HUMAN
US-60-173-469-1652

Query Match      27.4%; Score 31; DB 26; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 35
Db 25 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 55

RESULT 7
US-60-160-203-4277
; Sequence 4277, Application US/60160203
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000116
; CURRENT APPLICATION NUMBER: US/60/160,203
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 6374
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4277
; LENGTH: 80
; TYPE: PRT
; ORGANISM: HUMAN
; NAME/KEY: VARIANT
; LOCATION: (1)...(80)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-203-4277

Query Match      27.4%; Score 31; DB 26; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 35
Db 7 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 37

RESULT 8
US-60-169-840-6274
; Sequence 6274, Application US/60169840
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000164
; CURRENT APPLICATION NUMBER: US/60/169,840
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 9628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6274
; LENGTH: 98
```

```
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: VARIANT
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-169-840-6274

Query Match      27.4%; Score 31; DB 26; Length 98;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 35
Db 24 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 54

RESULT 9
US-08-124-469-19
; Sequence 19, Application US/08124469
; GENERAL INFORMATION:
; APPLICANT: RAPOPORT, Basil
; APPLICANT: MCLACHLAN, Sandra M.
; TITLE OF INVENTION: GRAVES' OPTHALMOPATHY ASSOCIATED
; TITLE OF INVENTION: ANTIBODIES, GRAVES' OPTHALMOPATHY ORBITAL ANTIGEN,
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR
; STREET: 1455 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/124,469
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 102.105.301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942-8400
; TELEFAX: (202)942-8484
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-124-469-19

Query Match      27.4%; Score 31; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 35
Db 5 TQSPSLPVTGPGEPAISCRSSQSLLHSNGY 35

RESULT 10
US-08-472-771-19
; Sequence 19, Application US/08472771
; GENERAL INFORMATION:
; APPLICANT: RAPOPORT, Basil
; APPLICANT: MCLACHLAN, Sandra M.
```



; SEQ ID NO 115  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-115

Query Match 27.4%; Score 31; DB 18; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.3e-22;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35  
|||||  
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

## RESULT 14

US-09-538-913-19  
; Sequence 19, Application US/09538913  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Paula  
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE  
; FILE REFERENCE: seqlist.DYX-15  
; CURRENT APPLICATION NUMBER: US/09/538,913  
; CURRENT FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-538-913-19

Query Match 27.4%; Score 31; DB 19; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.3e-22;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35  
|||||  
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

## RESULT 15

US-09-822-698A-19  
; Sequence 19, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 19  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: light chain variable region from a DPK 15 germ line  
US-09-822-698A-19

Query Match 27.4%; Score 31; DB 22; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.3e-22;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35  
|||||  
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35



GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:45 ; Search time 14.9898 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-1  
Perfect score: 113  
Sequence: 1 EIVLTQSPVLPVTPGEPAS.....MQGLQSPFTGPGTKVDIKR 113

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1006125 seqs, 276659714 residues

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Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
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2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	54	47.8	112	5	US-09-791-537-110202		Sequence 110202,
2	37	32.7	138	1	PCT-US02-09694-52		Sequence 52, Appl
3	32	28.3	118	5	US-09-791-537-54839		Sequence 54839, A
4	31	27.4	99	6	US-10-041-860-323		Sequence 323, App
5	31	27.4	99	6	US-10-041-860-365		Sequence 365, App
6	31	27.4	100	1	PCT-US02-12202-24		Sequence 24, Appl
7	31	27.4	100	5	US-09-791-537-24898		Sequence 24898, A
8	31	27.4	100	6	US-10-025-687-24		Sequence 24, Appl
9	31	27.4	100	6	US-10-153-382-38		Sequence 38, Appl
10	31	27.4	100	6	US-10-125-687-24		Sequence 24, Appl
11	31	27.4	100	6	US-10-041-860-8		Sequence 8, Appl
12	31	27.4	100	6	US-10-041-860-280		Sequence 280, App
13	31	27.4	100	6	US-10-041-860-321		Sequence 321, App
14	31	27.4	100	6	US-10-041-860-364		Sequence 364, App
15	31	27.4	100	6	US-10-010-942B-7		Sequence 7, Appl
16	31	27.4	109	5	US-09-791-537-88611		Sequence 88611, A
17	31	27.4	110	5	US-09-791-537-109684		Sequence 109684,
18	31	27.4	111	6	US-10-041-860-45		Sequence 45, Appl
19	31	27.4	111	6	US-10-041-860-219		Sequence 219, App
20	31	27.4	111	6	US-10-041-860-253		Sequence 253, App
21	31	27.4	111	6	US-10-041-860-363		Sequence 363, App
22	31	27.4	112	5	US-09-791-537-21281		Sequence 21281, A
23	31	27.4	112	5	US-09-791-537-21285		Sequence 21285, A
24	31	27.4	112	5	US-09-791-537-85986		Sequence 85986, A
25	31	27.4	113	1	PCT-US02-12202-9		Sequence 9, Appl
26	31	27.4	113	5	US-09-791-537-59499		Sequence 59499, A

27	31	27.4	113	6	US-10-025-687-9	Sequence 9, Appl
28	31	27.4	113	6	US-10-125-687-9	Sequence 9, Appl
29	31	27.4	113	6	US-10-041-860-30	Sequence 30, Appl
30	31	27.4	113	6	US-10-041-860-221	Sequence 221, App
31	31	27.4	113	6	US-10-041-860-255	Sequence 255, App
32	31	27.4	114	5	US-09-791-537-64706	Sequence 64706, A
33	31	27.4	114	5	US-09-791-537-86001	Sequence 86001, A
34	31	27.4	114	5	US-09-791-537-86326	Sequence 86326, A
35	31	27.4	114	5	US-09-791-537-122965	Sequence 122965,
36	31	27.4	114	5	US-09-791-537-137519	Sequence 137519,
37	31	27.4	114	6	US-10-041-860-322	Sequence 322, App
38	31	27.4	115	5	US-09-791-537-137518	Sequence 137518,
39	31	27.4	116	5	US-09-791-537-43479	Sequence 43479, A
40	31	27.4	116	5	US-09-791-537-104602	Sequence 104602,
41	31	27.4	117	5	US-09-791-537-48291	Sequence 48291, A
42	31	27.4	117	5	US-09-791-537-107503	Sequence 107503,
43	31	27.4	118	5	US-09-791-537-129360	Sequence 129360,
44	31	27.4	123	5	US-09-791-537-71832	Sequence 71832, A
45	31	27.4	125	6	US-10-010-942B-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-09-791-537-110202  
; Sequence 110202, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO. 110202  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-110202

Query Match 47.8%; Score 54; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 4.2e-42;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPCQSPOLLIY 54  
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPCQSPOLLIY 54

RESULT 2  
PCT-US02-09694-52

; Sequence 52, Application PC/TUS0209694  
; GENERAL INFORMATION:  
; APPLICANT: GERSHWIN, M. ERIC  
; TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY  
; FILE REFERENCE: ABX-UCD PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/09694  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human mAb  
; NAME/KEY: MOD\_RES

; LOCATION: (10)  
; OTHER INFORMATION: Any amino acid  
; NAME/KEY: MOD\_RES  
; LOCATION: (130)  
; OTHER INFORMATION: Any amino acid  
PCT-US02-09694-52

Query Match 32.7%; Score 37; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 2.5e-26;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PASISCRSSQSLHSGTYLDWYLRKPGSPQLLIY 54  
|||||  
DB 11 PASISCRSSQSLHSGTYLDWYLRKPGSPQLLIY 47

RESULT 3

US-09-791-537-54839  
; Sequence 54839, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 54839  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-54839

Query Match 28.3%; Score 32; DB 5; Length 118;  
Best Local Similarity 100.0%; Pred. No. 9e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLTQSPSLPVTGPGEASISCRSSQSLHSG 34  
|||||  
DB 5 VLTQSPSLPVTGPGEASISCRSSQSLHSG 36

RESULT 4

US-10-041-860-323  
; Sequence 323, Application US/10041860  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadl  
; APPLICANT: Weber, Richard  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; FILE REFERENCE: ARGENTIX 051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 323  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-323

Query Match 27.4%; Score 31; DB 6; Length 99;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TQSPSLPVTGPGEASISCRSSQSLHSGY 35  
|||||  
DB 5 TQSPSLPVTGPGEASISCRSSQSLHSGY 35

RESULT 5

US-10-041-860-365  
; Sequence 365, Application US/10041860  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadl  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
; FILE REFERENCE: ARGENTIX 051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 365  
; LENGTH: 99  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; NAME/KEY: VARIANT  
; LOCATION: 43, 58, 96  
; OTHER INFORMATION: Xaa = Any Amino Acid  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 43, 58, 96  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-041-860-365

Query Match 27.4%; Score 31; DB 6; Length 99;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHSGY 35  
|||||  
DB 5 TQSPSLPVTGPGEASISCRSSQSLHSGY 35

RESULT 6

PCT-US02-12202-24  
; Sequence 24, Application PC/TUS0212202  
; GENERAL INFORMATION:  
; APPLICANT: Abmaxis, Inc.  
; APPLICANT: Luo, Peizhi  
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY  
; FILE REFERENCE: 26050-706  
; CURRENT APPLICATION NUMBER: PCT/US02/12202  
; CURRENT FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-12202-24

Query Match 27.4%; Score 31; DB 1; Length 100;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

RESULT 12
US-10-041-860-280
; Sequence 280, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-280

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35
   |||||
Db 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

RESULT 13
US-10-041-860-321
; Sequence 321, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-321

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35
   |||||
Db 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

RESULT 14
US-10-041-860-364
; Sequence 364, Application US/10041860

```

```

; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 364
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-364

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35
   |||||
Db 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

RESULT 15
US-10-010-942B-7
; Sequence 7, Application US/10010942B
; GENERAL INFORMATION:
; APPLICANT: Basl, Gurid
; APPLICANT: Saidanah, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-942B-7

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35
   |||||
Db 5 TQSPSLPVTGPGEASISCRSSQSLHNSGY 35

Search completed: October 9, 2002, 19:33:55
Job time : 15.9898 secs

```



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:19:35 ; Search time 6.05357 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-1  
 perfect score: 113  
 Sequence: 1 ETVLTOSPISLPLVTPGEPAS.....MOGLOSPFTFGPCTKVDIKR 113

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length:	200000000
Maximum DB seq length:	200000000

Post-processing: Listing first 45 summaries

Database : PIR 71:\*

```

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	31	27.4	112	2	S58207	Ig light chain V r
2	31	27.4	112	2	S58206	Ig light chain V r
3	31	27.4	117	1	K2HUGM	Ig kappa chain pre
4	31	27.4	123	2	S40319	Ig kappa chain V r
5	31	27.4	132	2	S26882	Ig kappa chain V r
6	31	27.4	135	2	S40342	Ig kappa chain - h
7	31	27.4	136	2	S40357	Ig kappa chain V-J
8	30	26.5	114	2	S40375	Ig kappa chain - h
9	28	24.8	113	1	K2HUTW	Ig kappa chain V-I
10	27	23.9	100	2	S24681	Ig kappa chain - h
11	27	23.9	125	2	S40356	Ig kappa chain - h
12	27	23.9	126	2	S40339	Ig kappa chain - h
13	26	23.0	112	1	K2HUML	Ig kappa chain V-I
14	26	23.0	121	2	S40371	Ig kappa chain - h
15	24	21.2	120	2	A49043	Ig kappa chain V r
16	23	20.4	115	1	K2HUCM	Ig kappa chain V-I
17	23	20.4	121	2	S24205	Ig kappa chain V r
18	23	20.4	127	2	S40323	Ig kappa chain - h
19	23	20.4	130	2	S40321	Ig kappa chain - h
20	22	19.5	87	2	S34091	Ig kappa chain V r
21	22	19.5	100	2	H33730	Ig kappa chain V r
22	22	19.5	112	1	KVMSS1	Ig kappa chain V r
23	22	19.5	112	1	S38716	Ig light chain V r
24	22	19.5	113	1	KVMS17	Ig kappa chain V r
25	22	18.5	116	2	S20708	Ig kappa chain V r
26	22	19.5	119	2	B27588	Ig kappa chain pre
27	22	19.5	119	2	A27588	Ig kappa chain pre
28	22	19.5	124	2	S03876	Ig kappa chain V-I
29	20	17.7	112	2	I26317	Ig kappa chain V r

## ALIGNMENTS

## RESULT 1

```

RESOLUT I
S58207
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Welshof, M.; Terness, P.; Stanescu, D.; Zeve, M.; Hain, C.H.; Doebel, S.; Breitlin
submitted to the EMBL data library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable regi
A:Reference number: S58206
A:Accession: S58207
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89056; NID:g929642; PID:g929643
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

```

Query Match 27.4%; Score 31; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.6e-24;  
Matches 31: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY**      5 TQPSLSLPVTPGEPASISCRSSQSLLH\$NGY 35  
          |||||  
**Dd**      5 TOSPLSLPVTGPGEPA\$SICR\$SSO\$LLH\$NGY 35  
          |||||

## RESULT 2

RESULT 2  
S58206  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C: Species: Homo sapiens (man)  
C: Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C: Accession: S58206  
R: Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitlin  
submitted to the EMBL Data Library, July 1995  
A: Description: Characterization of heavy and light chain immunoglobulin variable regi  
A: Reference number: S58206  
A: Accession: S58206  
A: Status: preliminary  
A: Molecule type: mRNA  
A: Residues: 1-112 <NLE>  
A: Cross-references: EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:g929641  
C: Superfamily: immunoglobulin V region; immunoglobulin homology  
C: Keywords: immunoglobulin  
F: 16-95/Domain: immunoglobulin homology <IMM>

Query Match	27.4%	Score 31;	DB 2;	Length 112;
Best Local Similarity	100.0%;	Pred. No. 1.6e-24;		
Matches 31.	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

OV 5 TOSPLSLPVTGPASPASISCRSSQSLLHNGY 35

```

Db 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
|||||
RESULT 3
K2HUGM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAP>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted

Query Match 27.4%; Score 31; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 9 TOSPLSLPVTGEPASISCRSSQSLHNSGY 39
|||||

RESULT 4
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40319
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40319; MUID:94080891
A:Accession: S40319
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 15 TOSPLSLPVTGEPASISCRSSQSLHNSGY 45
|||||

RESULT 5
S26882
Ig kappa chain V region (V607) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

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C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combrato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882; MUID:90370099
A:Accession: S26882
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X52428; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 25 TOSPLSLPVTGEPASISCRSSQSLHNSGY 55
|||||

RESULT 6
S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40342; MUID:94080891
A:Accession: S40342
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: EMBL:X72452; NID:g441372; PID:g441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 18 TOSPLSLPVTGEPASISCRSSQSLHNSGY 48
|||||

RESULT 7
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40357; MUID:94080891
A:Accession: S40357
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 136;

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```

Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSGY 35
|||||
Db 25 TQSPSLPVTGPEPASISCRSSQSLHSGY 55

RESULT 8
S40375
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40375
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40375
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <KLE>
A:Cross-references: EMBL:X72485; NID:g441438; PIDN:CAA51153.1; PID:g441439
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 26.5%; Score 30; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSG 34
|||||
Db 2 TQSPSLPVTGPEPASISCRSSQSLHSG 31

RESULT 9
K2HUTW
Ig kappa chain V-II region (Tew) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A90370; A92764; A01888
R:Putnam, F.W.; Whitley, Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis
A:Reference number: A90370; MUID:74148480
A:Contents: Bence Jones protein Tew
A:Accession: A90370
A:Molecule type: protein
A:Residues: 1-113 <PUP>
A:Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia
A:Note: the C region of this chain has the Inv (L,2) marker
R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glennner, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with primary amyloidosis
A:Reference number: A92764; MUID:73166638
A:Contents: amyloid protein Tew
A:Accession: A92764
A:Molecule type: protein
A:Residues: 1-27 <TER>
A:Note: the major amyloid protein appears to be identical with the Bence Jones protein in amyloidosis
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 24.8%; Score 28; DB 1; Length 113;

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```

Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHLS 32
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLHLS 32

RESULT 10
S24681
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24681
R:van Es, J.H.
Submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24681
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <VAN>
A:Cross-references: EMBL:X67904; NID:g33435; PIDN:CAA48102.1; PID:g33436
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 27; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLH 31
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLH 31

RESULT 11
S40356
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40356
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40356
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 27; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLH 31
|||||
Db 14 TQSPSLPVTGPEPASISCRSSQSLH 40

RESULT 12
S40339
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40339
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891

```

```
A:Accession: S40339
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match      23.9%; Score 27; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5  TQSPSLPVTGPEPASISCRSSQSLH 31
      |||||
Db   20 TQSPSLPVTGPEPASISCRSSQSLH 46

RESULT 13
K2HUML
Ig kappa chain V-II region (M1) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01887
R:Dreyer, W.J.; Gray, W.R.; Hood, L.
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967
A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts and
A:Reference number: A01887
A:Accession: A01887
A:Molecule type: protein
A:Residues: 1-112 <DRE>
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB: IGV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match      23.0%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  IVLTQSPSLPVTGPEPASISCRSSQ 27
      |||||
Db   2  IVLTQSPSLPVTGPEPASISCRSSQ 27

RESULT 14
S40371
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40371
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40371
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-92/Domain: immunoglobulin homology <IMM>

Query Match      23.0%; Score 26; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  IVLTQSPSLPVTGPEPASISCRSSQ 27
      |||||
Db   2  IVLTQSPSLPVTGPEPASISCRSSQ 27
```

```
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5  TQSPSLPVTGPEPASISCRSSQSL 30
      |||||
Db   2  TQSPSLPVTGPEPASISCRSSQSL 27

RESULT 15
A49043
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49043
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.;
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A r
A:Reference number: A49043; MUID:92201291
A:Accession: A49043
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Note: sequence extracted from NCBI backbone (NCBIN:92557, NCBI:92565)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      21.2%; Score 24; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15  PGEPASISCRSSQSLHNGYTYL 38
      |||||
Db   35  PGEPASISCRSSQSLHNGYTYL 58

Search completed: October 9, 2002, 19:25:51
Job time : 6.05357 secs
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:13:25 : Search time 3.45918 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-1  
Perfect score: 113  
Sequence: 1 EVILTSPLSLPVTGPAPAS.....MOGLSQPFTFGTKVDIKR 113

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	27.4	117	1 KV2E_HUMAN	P06309 homo sapien
2	28	24.8	113	1 KV2D_HUMAN	P01617 homo sapien
3	26	23.0	112	1 KV2C_HUMAN	P01616 homo sapien
4	23	20.4	115	1 KV2A_HUMAN	P01614 homo sapien
5	22	19.5	112	1 KV2E_MOUSE	P01629 mus musculus
6	22	19.5	113	1 KV2E_MOUSE	P03976 mus musculus
7	20	17.7	113	1 KV2F_HUMAN	P01630 mus musculus
8	17	15.0	133	1 KV2F_HUMAN	P06310 homo sapien
9	14	12.4	108	1 KV1_CANFA	P01618 canis famil
10	13	11.5	107	1 KV1D_HUMAN	P01596 homo sapien
11	11	9.7	113	1 KV2B_HUMAN	P01615 homo sapien
12	11	9.7	113	1 KV2G_MOUSE	P01631 mus musculus
13	10	8.8	109	1 KV1F_HUMAN	P04208 homo sapien
14	10	8.8	109	1 KV2E_HUMAN	P01708 homo sapien
15	10	8.8	111	1 LV1A_HUMAN	P01699 homo sapien
16	10	8.8	111	1 LV2F_HUMAN	P01709 homo sapien
17	10	8.8	111	1 LV2G_HUMAN	P01710 homo sapien
18	10	8.8	111	1 LV2I_HUMAN	P01712 homo sapien
19	10	8.8	111	1 LV6C_HUMAN	P06317 homo sapien
20	10	8.8	112	1 LV1B_HUMAN	P01700 homo sapien
21	10	8.8	112	1 LV6A_HUMAN	P01721 homo sapien
22	10	8.8	114	1 KV4A_HUMAN	P01625 homo sapien
23	10	8.8	120	1 KV2B_MOUSE	P01627 mus musculus
24	10	8.8	121	1 KV40_HUMAN	P06312 homo sapien
25	10	8.8	133	1 KV4B_HUMAN	P06313 homo sapien
26	10	8.8	134	1 KV4C_HUMAN	P06314 homo sapien
27	9	8.0	108	1 KV5P_MOUSE	P01649 mus musculus
28	9	8.0	112	1 KV2A_MOUSE	P01628 mus musculus
29	9	8.0	113	1 KV2C_MOUSE	P01628 mus musculus
30	9	8.0	131	1 LV6E_HUMAN	P06319 homo sapien
31	8	7.1	100	1 KV3C_HUMAN	P01621 homo sapien
32	8	7.1	107	1 KV6A_MOUSE	P01675 mus musculus
33	8	7.1	107	1 KV6B_MOUSE	P01676 mus musculus

34	8	7.1	107	1 KV6C_MOUSE	P01677 mus musculus
35	8	7.1	107	1 KV6D_MOUSE	P01678 mus musculus
36	8	7.1	107	1 KV6E_MOUSE	P01679 mus musculus
37	8	7.1	108	1 KV1E_HUMAN	P01597 homo sapien
38	8	7.1	108	1 KV1Y_HUMAN	P03622 homo sapien
39	8	7.1	109	1 KV3B_HUMAN	P01620 homo sapien
40	8	7.1	109	1 KV3D_HUMAN	P01622 homo sapien
41	8	7.1	109	1 KV3E_HUMAN	P01623 homo sapien
42	8	7.1	109	1 KV3G_HUMAN	P04206 homo sapien
43	8	7.1	111	1 LV6D_HUMAN	P06318 homo sapien
44	8	7.1	112	1 LV1H_HUMAN	P06887 homo sapien
45	8	7.1	115	1 KV31_HUMAN	P04433 homo sapien

ALIGNMENTS

RESULT 1  
KV2E\_HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain diversity";  
RL Nature 309:73-76(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; Z00009; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A01889; K2HUGM.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.  
FT DOMAIN 5 27 FRAMEWORK-1.  
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 44 58 FRAMEWORK-2.  
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 66 97 FRAMEWORK-3.  
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 107 116 FRAMEWORK-4.  
FT DISULFID 27 97 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 27.4%; Score 31; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.8e-25;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPAPASICRSSQSLHNSGY 35  
|||||  
Db 9 TQSPSLPVTGPAPASICRSSQSLHNSGY 39  
|||||

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RESULT 2
KV2D_HUMAN  STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN PIR: A01888; K2HUM.
RP InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 24.8%; Score 28; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPASICRSQSLHLS 32
Db 5 TQSPSLPVTGPGEPASICRSQSLHLS 32

RESULT 3
KV2C_HUMAN  STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN PIR: A01888; K2HUM.
RP InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 24.8%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVLTQSPSLPVTGPGEPASICRSQ 27
Db 2 IVLTQSPSLPVTGPGEPASICRSQ 27

RESULT 4
KV2A_HUMAN  STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN PIR: A01888; K2HUCM.
RP InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 20.4%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;

```

```

[1]
RN PIR: A01888; K2HUM.
RP InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 23.0%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVLTQSPSLPVTGPGEPASICRSQ 27
Db 2 IVLTQSPSLPVTGPGEPASICRSQ 27

RESULT 4
KV2A_HUMAN  STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN PIR: A01888; K2HUCM.
RP InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 20.4%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;

```

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PLSLPVTPGEPASISCRSSQSLL 30  
 DB 9 PLSLPVTPGEPASISCRSSQSLL 31

## RESULT 5

KV2D\_MOUSE  
 ID KV2D\_MOUSE STANDARD; PRT; 112 AA.  
 AC P01629;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 2S1.3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83055101; PubMed=7141411;  
 RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;  
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for  
 the group A streptococcal polysaccharide."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).  
 CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
 ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
 DR PIR: A01911; KVMSS1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Monoclonal antibody.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;

Query Match 19.5%; Score 22; DB 1; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 SGTDFTLRISRVEAEDGVVYC 93  
 DB 72 SGTDFTLRISRVEAEDGVVYC 93

## RESULT 6

KV2E\_MOUSE  
 ID KV2E\_MOUSE STANDARD; PRT; 113 AA.  
 AC P03976;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 17S29.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85128968; PubMed=6441768;  
 RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;  
 RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6  
 origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the

RT group A-streptococcal polysaccharide.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).  
 CC -I- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.  
 DR PIR: A01912; KVMSS17.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 19.5%; Score 22; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-16;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 SGTDFTLRISRVEAEDGVVYC 93  
 DB 72 SGTDFTLRISRVEAEDGVVYC 93

## RESULT 7

KV2F\_MOUSE  
 ID KV2F\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01630;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE Ig kappa chain V-II region 7S34.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83256427; PubMed=6409088;  
 RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;  
 RT "A new isotype sequence (V kappa 27) of the variable region of kappa-  
 light chains from a mouse hybridoma-derived anti-(streptococcal group  
 A polysaccharide) antibody containing an additional cysteine residue.  
 Application of the dimethylaminoazobenzene isothiocyanate technique  
 for the isolation of peptides.";  
 RL Biochem. J. 211:173-180(1983).  
 CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  
 ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.  
 DR PIR: A01913; KVMSS7S.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT DOMAIN 40 54  
 FT DOMAIN 55 61  
 FT DOMAIN 62 93  
 FT DOMAIN 94 102  
 FT DOMAIN 103 112  
 FT DISULFID 23 93  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 17.7%; Score 20; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 76 FTLRISRVAEADVGVYCMQ 95
DB 76 FTLRISRVAEADVGVYCMQ 95

RESULT 8
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z00020; CAA77315.1; -.
DR PIR: A01890; K2HURP.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 15.0%; Score 17; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 80 ISRVEADVGVYCMQ 96
DB 100 ISRVEADVGVYCMQ 116

RESULT 9
KVL_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region GOM.
OS * Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunochimistry 15:303-305(1978).
CC -!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR: A01907; K2DGM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 12.4%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PGPASISCRSSQS 28
DB 15 PGPASISCRSSQS 28

RESULT 10
KVLD_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR HSSP; P80362; IWTLL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 N-LINKED (GLCNAC. . .).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

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Query Match      11.5%; Score 13; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 FTFEGTKVDIKR 113
DB 95 FTFEGTKVDIKR 107

RESULT 11
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUFF.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match      9.7%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AEDVGYYCMQ 95
DB 85 AEDVGYYCMQ 95

RESULT 12
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;

"Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVMS26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match      9.7%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQSL 29
DB 19 ASISCRSSQSL 29

RESULT 13
LV1F_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; L1HWA.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109
FT DISULFID 22 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match      8.8%; Score 10; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPRFSGS 70
DB 57 SGVPRFSGS 66

RESULT 14

```

Search completed: October 9, 2002, 19:23:36  
Job time : 3.45918 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 9.65689 seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-1  
Perfect score: 113  
Sequence: 1 EIVLTQSPLSLPTPGEPAS.....MGLQSPFTFGTKVDIKR 113

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mbc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	15.0	114	4 Q9UL80	Q9ul80 homo sapien
2	14	12.4	108	4 Q9UL83	Q9ul83 homo sapien
3	13	11.5	109	4 Q9UL86	Q9ul86 homo sapien
4	11	9.7	104	11 Q9UL82	Q9ul82 mus musculus
5	11	9.7	116	4 Q96PF6	Q96pf6 homo sapien
6	10	8.8	107	4 Q9UL81	Q9ul81 homo sapien
7	10	8.8	108	4 Q96SB0	Q96sb0 homo sapien
8	10	8.8	112	4 Q96JD2	Q96jd2 homo sapien
9	10	8.8	112	4 Q96JD1	Q96jd1 homo sapien
10	10	8.8	116	4 Q96JD0	Q96jd0 homo sapien
11	10	8.8	235	11 Q9LW12	Q9lw12 mus musculus
12	10	8.8	236	4 Q96E61	Q96e61 homo sapien
13	10	8.8	238	11 Q9M37	Q9m37 mus musculus
14	8	7.1	97	11 Q9UL76	Q9ul76 mus musculus
15	8	7.1	109	4 Q9UL78	Q9ul78 homo sapien
16	8	7.1	480	4 Q96JV4	Q96jv4 homo sapien

17	7	6.2	99	11	Q9JL74	Q9jl74 mus musculus
18	7	6.2	106	5	Q9U410	Q9u410 schistosoma
19	7	6.2	107	4	Q9NSD6	Q9nsd6 homo sapien
20	7	6.2	107	4	Q96SA9	Q96sa9 homo sapien
21	7	6.2	107	11	Q9ERZ9	Q9erz9 mus musculus
22	7	6.2	108	4	Q9UL79	Q9ul79 homo sapien
23	7	6.2	108	4	Q9UL77	Q9ul77 homo sapien
24	7	6.2	108	4	Q9UL70	Q9ul70 homo sapien
25	7	6.2	111	11	Q920E9	Q920e9 mus musculus
26	7	6.2	116	16	Q92CR3	Q92cr3 listeria in
27	7	6.2	130	4	Q9NP29	Q9np29 homo sapien
28	7	6.2	159	16	Q9RXF4	Q9rxf4 deinococcus
29	7	6.2	164	5	Q9GN43	Q9gn43 schistosoma
30	7	6.2	186	17	Q9HJE4	Q9hj4 thermoplasma
31	7	6.2	214	11	Q9CRX7	Q9crx7 mus musculus
32	7	6.2	218	11	Q925S1	Q925s1 mus musculus
33	7	6.2	258	2	Q933Q6	Q933q6 shigella fl
34	7	6.2	265	2	Q9WX68	Q9wx68 acetobacter
35	7	6.2	330	10	Q9FM86	Q9fm86 arabidopsis
36	7	6.2	337	2	Q9RJB9	Q9rjb9 streptomyce
37	7	6.2	343	16	Q92YC2	Q92yc2 rhizobium m
38	7	6.2	408	16	Q34765	Q34765 bacillus su
39	7	6.2	443	5	Q9GR71	Q9gr71 leishmania
40	7	6.2	516	3	Q9P340	Q9p340 penicillium
41	7	6.2	581	10	Q9XEK4	Q9xek4 brassica na
42	7	6.2	600	10	Q9SZ13	Q9sz13 arabidopsis
43	7	6.2	763	4	Q9UPX0	Q9upx0 homo sapien
44	7	6.2	801	2	Q9EUH6	Q9euh6 salmonella
45	7	6.2	802	2	Q9EUK1	Q9euk1 salmonella

#### ALIGNMENTS

RESULT 1

Q9UL80	PRELIMINARY;	PRT;	114 AA.
ID	Q9UL80		
AC	Q9UL80;		
DT	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).		
DE	OS Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035034; AAD56270.1; -.		
DR	HSSP; P80362; IWLTL.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IGV; 1.		
FT	NON_TER 1		
FT	NON_TER 114 114		
SQ	SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;		

Query Match 80 ISRVEAEDEVGYCYCMQ 96  
Best Local Similarity 100.0%; Score 17; DB 4; Length 114;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 ISRVEAEDEVGYCYCMQ 96  
Db 80 ISRVEAEDEVGYCYCMQ 96

```

RESULT 2
Q9UL83 .
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P80362; lWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 12.4%; Score 14; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 PFTGPGTKVDIKR 113
Db 95 PFTGPGTKVDIKR 108

RESULT 3
Q9UL86 .
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P80362; lWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match 11.5%; Score 13; DB 4; Length 109;

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Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 FTFGPGTKVDIKR 113
Db 97 FTFGPGTKVDIKR 109

RESULT 4
Q9JL82 .
ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSP; P01607; lREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFDF5F0AALAE CRC64;

Query Match 9.7%; Score 11; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ASISCRSSQSL 29
Db 11 ASISCRSSQSL 21

RESULT 5
Q96PF6 .
ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Conenno R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1
FT NON_TER 116 116

```

SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;  
 Query Match 9.7%; Score 11; DB 4; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 0.00045;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 PFTGPGTKVD 110  
 |||||  
 Db 95 PFTGPGTKVD 105

RESULT 6  
 ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035033; AAD56269.1; -;  
 DR HSP: P01607; IREI;  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 8.8%; Score 10; DB 4; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.0053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TFGPGTKVDI 111  
 |||||  
 Db 96 TFGPGTKVDI 105

RESULT 7  
 ID Q96SB0 PRELIMINARY; PRT; 108 AA.  
 AC Q96SB0;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN  
 DE VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adelson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyreactive monoclonal antibodies from  
 rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 antibody V region genes.";  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL: U96394; AAB68783.1; -;

FT NON\_TER 1  
 SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;  
 Query Match 8.8%; Score 10; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.0054;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70  
 |||||  
 Db 57 SGVPDRFSGS 66

RESULT 8  
 ID Q96JD2 PRELIMINARY; PRT; 112 AA.  
 AC Q96JD2;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
 RT "Amyloid lambda 6 light chain variable region NEG.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF267873; AAK58585.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 112  
 SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match 8.8%; Score 10; DB 4; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.0056;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70  
 |||||  
 Db 57 SGVPDRFSGS 66

RESULT 9  
 ID Q96JD1 PRELIMINARY; PRT; 112 AA.  
 AC Q96JD1;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
 RT "Amyloid lambda 6 light chain variable region PIP.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF267874; AAK58586.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 112  
 SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 8.8%; Score 10; DB 4; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 0.0056;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70  
 |||||

```
Db 57 SGVDRFSGS 66
RESULT 10
Q96JD0 PRELIMINARY; PRT; 116 AA.
AC Q96JD0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Perletti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region SAR.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF267875; AAK58587.1; -.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 8.8%; Score 10; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 SGVDRFSGS 70
Db 57 SGVDRFSGS 66

RESULT 11
Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 8.8%; Score 10; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 SGVDRFSGS 70
Db 77 SGVDRFSGS 86

RESULT 12
Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17259).
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 8.8%; Score 10; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 SGVDRFSGS 70
Db 77 SGVDRFSGS 86

RESULT 13
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00250; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 8.8%; Score 10; DB 11; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ASISCRSSQS 28
Db 38 ASISCRSSQS 47

RESULT 14
Q9JL76 PRELIMINARY; PRT; 97 AA.
AC Q9JL76;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2;  
 RA MEDLINE=20448942; PubMed=1092488;  
 RX Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-Cell-dependent antibody response to the dominant epitope of  
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin";  
 RL Infect. Immun. 68:5803-5808(2000).  
 DR EMBL; AF206030; AAF69328.1; -;  
 DR HSPF; P01679; 2FBJ.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 97  
 SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match 7.1%; Score 8; DB 11; Length 97;

Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ISRVEAED 87  
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 Db 64 ISRVEAED 71

# RESULT 15

Q9UL78 PRELIMINARY; PRT; 109 AA.  
 AC Q9UL78;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035036; AAD56272.1; -;  
 DR HSPF; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C5EC7EE197 CRC64;

Query Match 7.1%; Score 8; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 0.86; 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSP 8  
 |||||  
 Db 1 EIVLTQSP 8

Search completed: October 9, 2002, 19:24:57  
 Job time : 10.6569 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:24 ; Search time 12.1071 Seconds  
(Without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-1  
Perfect score: 592  
Sequence: 1 EIVLQSPSLPVTPEPAS.....MQGLQSPFTRPGTKGVDIR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :			
A.Geneseq_032802.*			
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2:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*	220	22
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4:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*	239	21
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9:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*	239	21
10:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*	239	21
11:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*	239	21
12:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*	239	21
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17:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*	239	21
18:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*	239	21
19:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*	239	21
20:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*	239	21
21:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*	239	21
22:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*	239	21

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	592	100.0	113 22	AAE12705 Human PH1 Fab anti
2	592	100.0	220 22	AAE12714 Human recombinant
3	592	100.0	381 22	AAE12707 Human b1vPH1-II-2
4	540	91.2	239 21	AAE12707 Human PTHR monocl
5	537	90.7	239 21	AAE12707 Human PTHR monocl
6	538	89.2	239 21	AAE12707 Human PTHR monocl
7	528	89.2	239 21	AAE12707 Human PTHR monocl
8	527	89.0	239 21	AAE12707 Human PTHR monocl
9	524	88.5	112 19	AAW53586 Light chain of a h
10	523.5	88.4	114 21	AAE12707 Anti-platelet glyc
11	523.5	88.4	131 21	AAE12707 Anti-platelet glyc

12	522	88.2	112	17	AAE12705	Human IgM GM607 va
13	521	88.0	239	21	AAE12705	Human PTHR monocl
14	520	87.8	239	21	AAE12705	Human PTHR monocl
15	519.5	87.8	113	21	AAE12705	Anti-platelet glyc
16	518.5	87.6	113	21	AAE12705	Anti-platelet glyc
17	517.5	87.4	112	21	AAE12705	Synthetic antibody
18	517.5	87.4	222	22	AAU04976	Synthetic antibody
19	517.5	87.4	222	22	AAU04976	Anti-HERF antibody
20	517.5	87.4	248	22	AAE12705	Anti-platelet glyc
21	512.5	86.6	111	21	AAE12705	Synthetic antibody
22	512.5	86.6	222	22	AAU04976	Human Ab light cha
23	511	86.3	109	20	AAE12705	Consensus single c
24	510	86.1	114	18	AAE12705	Amino acid sequenc
25	510	86.1	281	18	AAE12705	Human anti-Rh(D) c
26	507	85.6	112	21	AAE12705	Human PTHR monocl
27	505	85.3	112	22	AAE12705	Anti-CMV monoclonal
28	504	85.1	239	21	AAE12705	Human Anti-CD4 ant
29	502	84.8	113	15	AAE12705	Human protein seq
30	501	84.6	112	19	AAE12705	Human PTHR monocl
31	501	84.6	139	22	AAE12705	Human PTHR monocl
32	497	84.0	239	21	AAE12705	IgM antibody CEM 1
33	497	84.0	239	21	AAE12705	IgM antibody CEM 1
34	488	82.4	143	20	AAE12705	IgM antibody CEM 1
35	487	82.3	148	20	AAE12705	Vikappa for antibo
36	484.5	81.8	113	17	AAE12705	Human ICR-8.1 v-k
37	483	81.6	116	19	AAE12705	Humanised murine a
38	483	81.6	116	19	AAE12705	Humanised murine a
39	483	81.6	116	20	AAE12705	Protein sequence o
40	483	81.6	116	21	AAE12705	Humanised ICR-8.1
41	483	81.6	116	21	AAE12705	Humanised murine a
42	483	81.6	116	21	AAE12705	Humanised MAB ligh
43	482	81.4	112	14	AAE12705	Mature light chain
44	482	81.4	112	18	AAE12705	Human Mab AB17.1.4
45	482	81.4	112	19	AAE12705	

ALIGNMENTS

RESULT 1	
AAE12705	
ID	AAE12705 standard; Protein; 113 AA.
XX	
AC	AAE12705;
XX	
DT	04-JAN-2002 (first entry)
XX	
DE	Human PH1 Fab antibody variable light chain region (VL).
XX	
KW	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma variable light chain region; cancer; breast; ovary; lung; bladder; cytostatic; therapy; PH1 antibody.
KW	
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Region
FT	
FT	Region
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XX PA (DYAX-) DYAX CORP.  
 XX PI Hoogenboom HRJM, Henderikx MPG;  
 XX DR WPI; 2001-626437/72.  
 XX DR N-PSDB; AAD20730.  
 XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member  
 XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
 XX PT its portion for binding to an epitope of the protein core of mucin-1 -  
 XX PS Claim 3; Page 93; 126pp; English.  
 XX CC The invention relates to an isolated tumour-associated antigen mucin-1  
 XX CC (MUC-1)-specific binding member comprising an antigen binding domain  
 XX CC region having an antibody variable light (VL) or heavy (VH) region,  
 XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific  
 XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma  
 XX CC The binding of MUC1-specific binding member to MUC1 is detected by a  
 XX CC detection method selected from enzyme-linked immunosorbent assay,  
 XX CC magnetic resonance imaging, scintillation counting, and X-ray film.  
 XX CC MUC1-specific binding member is useful for treating cancer, preferably  
 XX CC adenocarcinoma, in an individual, where the cancer is present in tissue  
 XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific  
 XX CC binding member is useful for diagnosing and imaging MUC1-expressing  
 XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,  
 XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-  
 XX CC containing molecules, and for therapeutically or prophylactically  
 XX CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab  
 XX CC antibody VL region.  
 XX SQ Sequence 113 AA;  
 Query Match 100.0%; Score 592; DB 22; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-42;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSNGVYLDWYIQKPGQSPQLLIYSGSHRA 60  
 Db 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSNGVYLDWYIQKPGQSPQLLIYSGSHRA 60  
 Qy 61 SGVPDRFSGVSGTDFTLRISRVEADVGYYCMOGLQSPFTFGPTGKVDIKR 113  
 Db 61 SGVPDRFSGVSGTDFTLRISRVEADVGYYCMOGLQSPFTFGPTGKVDIKR 113  
 RESULT 2  
 AAE12714  
 ID AAE12714 standard; Protein; 220 AA.  
 XX AC AAE12714;  
 XX DT 04-JAN-2002 (first entry)  
 XX DE Human recombinant immunoglobulin (Ig) light chain region.  
 XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;  
 XX KW light chain region; cancer; breast; ovary; lung; bladder;  
 XX KW cytostatic; therapy; immunoglobulin; Ig.  
 XX OS Homo sapiens.  
 XX PN WO200175110-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US10589.  
 XX PR 30-MAR-2000; 2000US-0538913.  
 XX PA (DYAX-) DYAX CORP.  
 XX PI Hoogenboom HRJM, Henderikx MPG;  
 XX DR WPI; 2001-626437/72.  
 XX DR N-PSDB; AAD20732.

PI Hoogenboom HRJM, Henderikx MPG;  
 XX WPI; 2001-626437/72.  
 XX DR N-PSDB; AAD20744.  
 XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member  
 XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
 XX PT its portion for binding to an epitope of the protein core of mucin-1 -  
 XX PS Claim 12; Page 103; 126pp; English.  
 XX CC The invention relates to an isolated tumour-associated antigen mucin-1  
 XX CC (MUC-1)-specific binding member comprising an antigen binding domain  
 XX CC region having an antibody variable light (VL) or heavy (VH) region,  
 XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific  
 XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma  
 XX CC The binding of MUC1-specific binding member to MUC1 is detected by a  
 XX CC detection method selected from enzyme-linked immunosorbent assay,  
 XX CC magnetic resonance imaging, scintillation counting, and X-ray film.  
 XX CC MUC1-specific binding member is useful for treating cancer, preferably  
 XX CC adenocarcinoma, in an individual, where the cancer is present in tissue  
 XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific  
 XX CC binding member is useful for diagnosing and imaging MUC1-expressing  
 XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,  
 XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-  
 XX CC containing molecules, and for therapeutically or prophylactically  
 XX CC treating cancer. The present sequence is human recombinant immunoglobulin  
 XX CC (Ig) light chain region (variable VL and CL constant kappa light chain).  
 XX SQ Sequence 220 AA;  
 Query Match 100.0%; Score 592; DB 22; Length 220;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-41;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSNGVYLDWYIQKPGQSPQLLIYSGSHRA 60  
 Db 1 EIVLTQSLPLVTPGEPASISCRSSQSLHNSNGVYLDWYIQKPGQSPQLLIYSGSHRA 60  
 Qy 61 SGVPDRFSGVSGTDFTLRISRVEADVGYYCMOGLQSPFTFGPTGKVDIKR 113  
 Db 61 SGVPDRFSGVSGTDFTLRISRVEADVGYYCMOGLQSPFTFGPTGKVDIKR 113  
 RESULT 3  
 AAE12707  
 ID AAE12707 standard; Protein; 381 AA.  
 XX AC AAE12707;  
 XX DT 04-JAN-2002 (first entry)  
 XX DE Human blyPHI-IL-2 immunocytokine protein.  
 XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;  
 XX KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.  
 XX OS Homo sapiens.  
 XX PN WO200175110-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US10589.  
 XX PR 30-MAR-2000; 2000US-0538913.  
 XX PA (DYAX-) DYAX CORP.  
 XX PI Hoogenboom HRJM, Henderikx MPG;  
 XX DR WPI; 2001-626437/72.  
 XX DR N-PSDB; AAD20732.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member  
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
PT its portion for binding to an epitope of the protein core of mucin-1  
XX  
PS Claim 9; Page 95-97; 126pp; English.  
XX  
CC The invention relates to an isolated tumour-associated antigen mucin-1  
CC (MUC-1)-specific binding member comprising an antigen binding domain  
CC region having an antibody variable light (VL) or heavy (VH) region,  
CC or a complementarily determining region (CDR) of VL or VH. MUC1-specific  
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma  
CC The binding of MUC1-specific binding member to MUC1 is detected by a  
CC detection method selected from enzyme-linked immunosorbent assay,  
CC magnetic resonance imaging, scintillation counting, and x-ray film.  
CC MUC1-specific binding member is useful for treating cancer, preferably  
CC adenocarcinoma, in an individual, where the cancer is present in tissue  
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific  
CC binding member is useful for diagnosing and imaging MUC1-expressing  
CC cancer cells and tissues, for purifying or isolating non-glycosylated,  
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-  
CC containing molecules, and for therapeutically or prophylactically  
CC treating cancer. The present sequence is human bivPH1-IL-2  
CC immunocytokine protein. bivPH1 is mucin specific binding portion.  
XX  
XX Sequence 381 AA;  
SQ  
Query Match 100.0%; Score 592; DB 22; Length 381;  
Best Local Similarity 100.0%; Pred. No. 2.7e-41;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTLDWYLKQKQSPQLLIYSGSHRA 60  
DB 127 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTLDWYLKQKQSPQLLIYSGSHRA 186  
QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113  
DB 187 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239  
RESULT 4  
AY82615  
ID AAY82615 standard; Protein; 239 AA.  
XX  
XX AAY82615;  
XX  
DT 02-AUG-2000 (first entry)  
DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.  
XX  
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 155  
FT /note= "possible Ala"  
FT  
XX JP2000080100-A.  
XX  
XX 21-MAR-2000.  
XX  
XX 12-OCT-1998; 98JP-0304793.  
XX  
XX 17-JUN-1998; 98JP-0188196.  
XX  
XX 26-JUN-1998; 98JP-0196729.  
XX  
XX (NIBS ) JAPAN TOBACCO INC.  
XX

DR WPI; 2000-286723/25.  
DR N-PSDB; AAA13925.  
XX  
PT A human monoclonal antibody to parathyroid hormone related protein. -  
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain  
XX  
XX Claim 31; Page 45-46; 88pp; Japanese.  
PS  
XX The present invention describes a human monoclonal antibody to  
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
XX its fragments, following the stimulation of PTHrP has the following  
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
XX the release of calcium from bone; or (c) inhibits elevation of blood  
XX calcium content. The monoclonal antibody can be used in the treatment  
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome  
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
XX antiinflammatory activities. The present sequence represents a  
XX human PTHrP monoclonal antibody clone protein sequence from the  
XX present invention.  
XX  
XX Sequence 239 AA;  
SQ  
Query Match 91.2%; Score 540; DB 21; Length 239;  
Best Local Similarity 90.3%; Pred. No. 3.2e-37;  
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTLDWYLKQKQSPQLLIYSGSHRA 60  
DB 21 DIVMTQSPSLSPVTPGEPASISCRSSQSLHNSGYTLDWYLKQKQSPQLLIYSGSHRA 80  
QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113  
DB 81 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 133  
RESULT 5  
AY82616  
ID AAY82616 standard; Protein; 239 AA.  
XX  
XX AAY82616;  
XX  
DT 02-AUG-2000 (first entry)  
DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.  
XX  
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 5  
FT /label= Val, Ala, Asp, Gly  
FT Misc-difference 13  
FT /note= "possibly Leu"  
FT Misc-difference 25  
FT /label= Ile, Thr, Asn, Ser  
FT Misc-difference 27  
FT /label= Phe, Ser, Tyr, Cys  
FT Misc-difference 216  
FT /note= "possible Val"  
XX  
XX JP2000080100-A.  
XX  
XX 21-MAR-2000.  
XX  
XX 12-OCT-1998; 98JP-0304793.  
XX





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XX OS Homo sapiens.
XX PN WO9810070-A1.
XX XX 12-MAR-1998.
XX PD 27-AUG-1997; 97WO-JP02983.
XX PF 20-SEP-1996; 96JP-0271546.
XX PR 02-SEP-1996; 96JP-0231742.
XX XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX PI Eda Y, Higuchi H, Maeda H, Nakata M, Okumura K;
XX PI Ushio Y;
XX XX WPI; 1998-193620/17.
XX XX Human immunoglobulin or its active fragment specific for Fas ligand
XX PT - for treatment of AIDS, organ rejection, autoimmune diseases e.g.
XX PT systemic lupus erythematosus and diabetes
XX XX Disclosure; Page 261; 348pp; Japanese.
XX XX The present sequence represents the light chain of a human antibody, and
XX CC can be used in the humanised immunoglobulin of the invention. The
XX CC humanised immunoglobulin reacts specifically with a region of a Fas
XX CC ligand that is important in inhibiting apoptosis induced by cells with
XX CC Fas expression. The immunoglobulin of the invention can inhibit
XX CC physiological reactions between a Fas ligand and Fas, typified by
XX CC apoptosis. The humanised immunoglobulin is used for treatment of AIDS,
XX CC rejection following transplant surgery, autoimmune diseases such as
XX CC SLE or RA, and diabetes.
XX XX Sequence 112 AA;
XX SQ Query Match 88.5%; Score 524; DB 19; Length 112;
XX Best Local Similarity 87.5%; Pred. No. 3.le-36;
XX Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIVLTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYLSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLQSPFTFGPGTKVDIK 112
DB 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQALQTPYTFGGQTKLEIK 112
RESULT 10
AAY95186
ID AAY95186 standard; Protein; 114 AA.
XX AC AAY95186;
XX XX 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human Hib-5 VL.
XX XX Variable light chain; single chain antibody; scFv; human; Hib-5;
XX KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX KW antithrombotic; thrombus; therapy; diagnostic.
XX XX Homo sapiens.
XX XX Key Location/Qualifiers
XX FH 1..23 /note= "framework region 1"
XX FT 24..39 /note= "complementarity determining region 1"
XX FT 40..54 /note= "framework region 2"
XX FT

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FT Region 55..61 /note= "complementarity determining region 2"
FT FT 62..93 /note= "framework region 3"
FT FT 94..101 /note= "complementarity determining region 3"
FT FT 102..114 /note= "framework region 4"
XX XX WO200026667-A1.
XX PN 11-MAY-2000.
XX PD 29-OCT-1999; 99WO-US25495.
XX PF 30-OCT-1998; 98US-0106275.
XX PR (MILL/) MILLER J L.
XX XX PI Miller JL;
XX XX WPI; 2000-365744/31.
XX DR N-PSDB; AAA27664.
XX XX Isolated nucleic acid molecule encoding anti-human platelet
XX PT glycoprotein Ib alpha molecule useful for producing antibodies which
XX PT inhibit platelet aggregation -
XX PS Claim 11; Page 77; 89pp; English.
XX XX The present sequence is that of the light chain variable region
XX CC (VL) of human single chain antibody (scFv) Hib-5, which is directed
XX CC against platelet glycoprotein Ib (GPib). The Hib series of scFv
XX CC was isolated from a human synthetic VH and VL scFv library by 3
XX CC rounds of phagemid selection against transfected CHO cells
XX CC expressing the GPib alpha component of the GPIb/IX/V complex
XX CC on their surface, followed by a 4th round of selection against
XX CC washed human platelets, and 2 final rounds in which attempts were
XX CC made to displace scFv from washed platelets by flooding with
XX CC murine monoclonal antibody or mimotope peptide (see AAY95229).
XX CC Whether displayed as surface proteins on a phagemid or secreted
XX CC as free scFv by Escherichia coli, the Hib scFv clones are capable
XX CC of inhibiting von Willebrand factor-dependent aggregation of
XX CC platelets. The scFv are composed of native human protein sequences
XX CC and are therefore attractive potential reagents for therapeutic
XX CC purposes. They provide a new class of antithrombotic agents,
XX CC useful for the prevention of platelet-dependent thrombi in
XX CC diseased arteries, bypass grafts, dialysis etc., and can also be
XX CC used as diagnostic reagents. Methods of inhibiting aggregation
XX CC of platelets, of binding human platelet GPIb alpha and of selecting
XX CC a VH or VL region of an antibody that inhibits platelet aggregation
XX CC are claimed.
XX SQ Sequence 114 AA;
XX Query Match 88.4%; Score 523.5; DB 21; Length 114;
XX Best Local Similarity 87.7%; Pred. No. 3.5e-36;
XX Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 EIVLTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYLSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQALQTPPTFGGQTKLEIKR 114
RESULT 11
AAY95226
ID AAY95226 standard; Protein; 131 AA.
XX XX AAY95226;
XX AC AAY95226;

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XX 29-AUG-2000 (first entry)  
 XX Anti-platelet glycoprotein Ib human H1b-5 VL region and linker.  
 XX  
 KW Variable light chain: single chain antibody; scFv; human; H1b-5;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.  
 XX  
 OS Chimeric - Synthetic.  
 OS Chimeric - Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Peptide 1..17 "vector-derived linker"  
 FT Region 18..131  
 FT Region 18..40 "light chain variable region"  
 FT Region 41..56 "framework region 1"  
 FT Region 57..71 "complementarity determining region 1"  
 FT Region 72..78 "framework region 2"  
 FT Region 79..110 "complementarity determining region 2"  
 FT Region 111..119 "framework region 3"  
 FT Region 120..131 "complementarity determining region 3"  
 FT Region 132..131 "framework region 4"  
 XX WO200026667-A1.  
 XX  
 XX 11-MAY-2000.  
 XX  
 XX 29-OCT-1999; 99WO-US25495.  
 XX  
 XX 30-OCT-1998; 98US-0106275.  
 XX  
 XX (MILLER) MILLER J L.  
 XX  
 XX MILLER JL;  
 XX  
 XX WPI: 2000-365744/31.  
 XX  
 XX Isolated nucleic acid molecule encoding anti-human platelet  
 XX glycoprotein Ib alpha molecule useful for producing antibodies which  
 XX inhibit platelet aggregation -  
 XX  
 XX Disclosure; Fig 8; 89pp; English.  
 XX  
 XX The present sequence is that of the light chain variable region  
 XX (VL) plus linker peptide of human single chain antibody (scFv)  
 XX H1b-5, which is directed against platelet glycoprotein Ib (GP1b).  
 XX H1b-5 is composed of a heavy chain variable region and light chain  
 XX variable region joined via a vector-derived peptide linker. The  
 XX H1b series of scFv was isolated from a human synthetic VH and VL  
 XX scFv library by 3 rounds of phagemid selection against transfected  
 XX CHO cells expressing the GP1b alpha component of the GP1b/IX/V  
 XX complex on their surface, followed by a 4th round of selection  
 XX against washed human platelets, and 2 final rounds in which  
 XX attempts were made to displace scFv from washed platelets by  
 XX flooding with murine monoclonal antibody or mimotope peptide (see  
 XX AA95229). Whether displayed as surface proteins on a phagemid or  
 XX secreted as free scFv by *Escherichia coli*, the H1b scFv clones are  
 XX capable of inhibiting von Willebrand factor-dependent aggregation of  
 XX platelets. The scFv are composed of native human protein sequences  
 XX and are therefore attractive potential reagents for therapeutic  
 XX purposes. They provide a new class of antithrombotic agents,  
 XX useful for the prevention of platelet-dependent thrombi in  
 XX diseased arteries, bypass grafts, dialysis etc., and can also be  
 XX used as diagnostic reagents. Methods of inhibiting aggregation

CC of platelets, of binding human platelet GP1b alpha and of selecting  
 CC a VH or VL region of an antibody that inhibits platelet aggregation  
 CC are claimed.  
 XX  
 SQ Sequence 131 AA;  
 Query Match 88.4%; Score 523.5; DB 21; Length 131;  
 Best Local Similarity 87.7%; Pred. NO. 4.1e-36;  
 Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 EIVLTQSPPLSLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYGSNRA 60  
 DB 18 DVMTQSPPLSLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPQLLIYGSNRA 77  
 QY 61 SGVPRFSGSVSGTDTFLIRSRVEAEADVGYVYCMQGLQS-PFTFGPTKVDIKR 113  
 DB 78 SGVPRFSGSVSGTDTFLIRSRVEAEADVGYVYCMQALQTPPTFGQTKLEIKR 131  
 RESULT 12  
 AAR95218  
 ID AAR95218 standard; protein; 112 AA.  
 XX  
 AC AAR95218;  
 XX  
 DT 16-DEC-1996 (first entry)  
 XX  
 DE Human IgM GM607 variable light chain.  
 XX  
 KW Antibody; fusion protein; single chain; inhibition; tumour;  
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;  
 KW immunosay; Lewis(X) carbohydrate antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 24..39  
 FT Domain /label= CDR 1.  
 FT Domain 55..61  
 FT Domain /label= CDR 2.  
 FT Domain 89..97  
 FT Domain /label= CDR 3.  
 XX  
 PN WO9613594-A1.  
 XX  
 XX 09-MAY-1996.  
 XX  
 XX 26-OCT-1995; 95WO-US13811.  
 XX  
 XX 28-OCT-1994; 94US-0331398.  
 XX 28-OCT-1994; 94US-0331396.  
 XX 28-OCT-1994; 94US-0331397.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;  
 XX Padlan EA, Pai L, Pastan I, Willingham M;  
 XX  
 XX WPI: 1996-251462/25.  
 XX  
 XX Single chain fusion proteins and antibodies - useful to diagnose and  
 XX treat cancer, specifically bind Lewis(X) related carbohydrate  
 XX antigen  
 XX  
 XX Example 13; Figure 11B; 116pp; English.  
 XX  
 XX A novel recombinant DNA molecule which encodes a single chain fusion  
 XX protein or antibody comprising the Fv region of both the light and  
 XX heavy chains of an antibody (Ab) fused together, and an effector  
 XX molecule, where the fusion protein or Ab has the binding specificity  
 XX of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production  
 XX of such fusion proteins or antibodies. The fusion proteins can be  
 XX used in compositions as an immunotoxin to inhibit tumour cell growth.

CC The single chain antibody can be used to detect the presence or  
 CC absence of cells bearing a Lewis(X) carbohydrate antigen in a  
 CC patient. The antibodies are also useful as multiple targeting  
 CC moieties, providing at least 2 kinds of biological activity. They  
 CC can also be used in diagnostic assays and for the imaging of tumours  
 CC when attached to a radiolabel and for the pathological diagnosis of  
 CC tumours. Humanised antibodies are less immunogenic than the mouse  
 CC Mabs B1, B3 and B5, making them more suitable for long term  
 CC treatment.

XX Sequence 112 AA;  
 SQ Query Match 88.2%; Score 522; DB 17; Length 112;  
 Best Local Similarity 89.3%; Pred. No. 4.6e-36;  
 Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWYLKQPGSQPQLLIYSGSHRA 60  
 DB 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWYLKQPGSQPQLLIYLSNRA 60  
 OY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPTKVDIK 112  
 DB 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQTPQTGGTKVEIK 112

RESULT 13  
 AAY82611  
 ID AAY82611 standard; Protein; 239 AA.  
 XX  
 AC AAY82611;  
 XX  
 DT 02-AUG-2000 (first entry)  
 DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:5.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2000080100-A.  
 XX  
 XX 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-0304793.  
 XX  
 PR 17-JUN-1998; 98JP-0188196.  
 PR 26-JUN-1998; 98JP-0196729.  
 XX  
 PA (NITSB ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13921.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain  
 XX  
 PS Claim 31; Page 34-35; 86pp; Japanese.  
 XX

CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and

CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.

XX Sequence 239 AA;  
 SQ Query Match 88.0%; Score 521; DB 21; Length 239;  
 Best Local Similarity 86.7%; Pred. No. 1.2e-35;  
 Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWYLKQPGSQPQLLIYSGSHRA 60  
 DB 21 DIVMTQSLPLVPTGEPATISCRSSQSLHNRNGNYLDWFLQKPGSQPQLLIYLSNRA 80  
 OY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPTKVDIKR 113  
 DB 81 SGVPDRFSGVSGTDFTLKLSRVEAEDGVLYVCMQALQPIPTFGPTKVDIKR 133

RESULT 14  
 AAY82614  
 ID AAY82614 standard; Protein; 239 AA.  
 XX  
 AC AAY82614;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 117 /label= Leu, Ile, Val  
 FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 216 /note= "possible Val"  
 XX  
 PN JP2000080100-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-0304793.  
 XX  
 PR 17-JUN-1998; 98JP-0188196.  
 PR 26-JUN-1998; 98JP-0196729.  
 XX  
 PA (NITSB ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13924.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain  
 XX  
 PS Claim 31; Page 43; 88pp; Japanese.  
 XX

CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits



CC the release of calcium from bone; or (c) inhibits elevation of blood  
CC calcium content. The monoclonal antibody can be used in the treatment  
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a  
CC human PTHR monoclonal antibody clone protein sequence from the  
CC present invention.

XX SQ Sequence 239 AA;

Query Match 87.8%; Score 520; DB 21; Length 239;  
Best Local Similarity 87.6%; Pred. No. 1.5e-35;  
Matches 99; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRA 60  
DB 21 DIVMXQXPLSLVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGSQPOLLIYLSNRA 80  
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPKTKVDIKR 113  
DB 81 SGVDPFRFSGSGTDFTLKISRVEAEDGVVYCMQAXQIFPTFGPKTKVDIKR 133

RESULT 15

AA95221  
ID AA95221 standard; Protein; 113 AA.

XX AC AA95221;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human Hib-5 VL.

XX KW Variable light chain; single chain antibody; scFv; human; Hib-5;  
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
XX antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..23  
FT /note= "framework region 1"  
FT Region 24..39  
FT /note= "complementarity determining region 1"  
FT Region 40..54  
FT /note= "framework region 2"  
FT Region 55..61  
FT /note= "complementarity determining region 2"  
FT Region 62..93  
FT /note= "framework region 3"  
FT Region 94..101  
FT /note= "complementarity determining region 3"  
FT Region 102..113  
FT /note= "framework region 4"

XX WO2000026667-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-US25495.

XX PR 30-OCT-1998; 98US-0106275.

XX PA (MILLER) MILLER J L.

XX PI Miller JL;

XX DR WPI: 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet  
PT glycoprotein Ib alpha molecule useful for producing antibodies which

PT inhibit platelet aggregation -  
XX  
PS Claim 18; Fig 8; 89pp; English.

XX The present sequence is that of the light chain variable region  
CC (VL) of human single chain antibody (scFv) Hib-5, which is directed  
CC against platelet glycoprotein Ib (GPiB). The Hib series of scFv  
CC was isolated from a human synthetic VH and VL scFv library by 3  
CC rounds of phagemid selection against transfected CHO cells  
CC expressing the GPiB alpha component of the GPiB/IX/V complex  
CC on their surface, followed by a 4th round of selection against  
CC washed human platelets, and 2 final rounds in which attempts were  
CC made to displace scFv from washed platelets by flooding with  
CC murine monoclonal antibody or mimotope peptide (see AA95229).  
CC Whether displayed as surface proteins on a phagemid or secreted  
CC as free scFv by Escherichia coli, the Hib scFv clones are capable  
CC of inhibiting von Willebrand factor-dependent aggregation of  
CC platelets. The scFv are composed of native human protein sequences  
CC and are therefore attractive potential reagents for therapeutic  
CC purposes. They provide a new class of antithrombotic agents,  
CC useful for the prevention of platelet-dependent thrombi in  
CC diseased arteries, bypass grafts, dialysis etc., and can also be  
CC used as diagnostic reagents. Methods of inhibiting aggregation  
CC of platelets, of binding human platelet GPiB alpha and of selecting  
CC a VH or VL region of an antibody that inhibits platelet aggregation  
CC are claimed.

CC Note: The present sequence is not shown in the specification but is  
CC derived from the Hib-5 VH sequence given in Fig 8 (see AA95220).

XX SQ Sequence 113 AA;

Query Match 87.8%; Score 519.5; DB 21; Length 113;  
Best Local Similarity 88.5%; Pred. No. 7.5e-36;  
Matches 100; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYSGSHRA 60

DB 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPOLLIYLSNRA 60

QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPKTKVDIKR 112  
DB 61 SGVDPFRFSGSGTDFTLKISRVEAEDGVVYCMQALQTPFTFGPKTKLEIK 113

Search completed: October 9, 2002, 19:10:27

Job time : 13.1071 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:09:15 ; Search time 4.61224 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-1  
Perfect score: 592  
Sequence: 1 EIVLTQSPLSLPVTGPEPAS.....MQGLQSPFTGPGKVKDIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep: \*  
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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep: \*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	532	89.9	113	4	US-09-025-769B-15	Sequence 15, Appl
2	522	88.2	112	1	US-08-331-398A-49	Sequence 49, Appl
3	522	88.2	112	2	US-08-331-397B-49	Sequence 49, Appl
4	522	88.2	112	2	US-08-759-804A-49	Sequence 49, Appl
5	522	88.2	112	4	US-09-227-693-49	Sequence 49, Appl
6	510	86.1	114	4	US-09-025-769B-29	Sequence 29, Appl
7	510	86.1	114	4	US-09-025-769B-45	Sequence 45, Appl
8	510	86.1	281	4	US-09-025-769B-178	Sequence 178, Appl
9	505	85.3	112	4	US-09-240-274-30	Sequence 30, Appl
10	502	84.8	113	1	US-08-082-623-4	Sequence 4, Appl
11	501	84.6	112	1	US-08-478-039-88	Sequence 88, Appl
12	501	84.6	112	1	US-08-478-039-88	Sequence 88, Appl
13	499	84.3	112	1	US-08-053-171-16	Sequence 16, Appl
14	484.5	81.8	113	1	US-08-264-093-10	Sequence 10, Appl
15	484	81.8	112	1	US-08-331-398A-50	Sequence 50, Appl
16	484	81.8	112	2	US-08-331-397B-50	Sequence 50, Appl
17	484	81.8	112	2	US-08-759-804A-50	Sequence 50, Appl
18	484	81.8	112	4	US-09-227-693-50	Sequence 50, Appl
19	483	81.6	116	1	US-08-482-882-66	Sequence 66, Appl
20	483	81.6	116	2	US-08-482-882-66	Sequence 66, Appl
21	483	81.6	116	2	US-08-487-113D-66	Sequence 66, Appl
22	483	81.6	116	2	US-08-473-503-66	Sequence 66, Appl
23	483	81.6	116	2	US-08-483-932-66	Sequence 66, Appl
24	483	81.6	116	2	US-08-720-420A-66	Sequence 66, Appl
25	483	81.6	116	3	US-08-714-017-66	Sequence 66, Appl
26	483	81.6	116	3	US-08-475-680-66	Sequence 66, Appl
27	482	81.4	112	1	US-08-053-171-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1  
US-09-025-769B-15  
; Sequence 15, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Illag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MOREHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-15

Query Match 89.9%; Score 532; DB 4; Length 113;  
Best Local Similarity 88.5%; Pred. No. 4.2e-43;  
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Sequence 14, Appl  
Sequence 2, Appl  
Sequence 95, Appl  
Sequence 50, Appl  
Sequence 95, Appl  
Sequence 151, App  
Sequence 151, App  
Sequence 13, Appl  
Sequence 15, Appl  
Sequence 151, App  
Sequence 151, App  
Sequence 151, App  
Sequence 89, Appl  
Sequence 89, Appl  
Sequence 67, Appl  
Sequence 67, Appl

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYSGSHRA 60  
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYLSGNRA 60

QY 61 SGVPDRFSGSGVSGTDFTLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113  
Db 61 SGVPDRFSGSGVSGTDFTLKISRVEADGVVYCMQALQTPVTFGQGPKEIKR 113

RESULT 2  
US-08-331-398A-49  
; Sequence 49, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pal, Lee  
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
; TITLE OF INVENTION: and Their Uses (as amended)  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331.398A  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-126110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
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; LOCATION: 1..112  
; OTHER INFORMATION: /note= "Human IgM antibody GM607  
; OTHER INFORMATION: Variable Light chain (V-L)"  
US-08-331-398A-49

Query Match 88.2%; Score 522; DB 1; Length 112;  
Best Local Similarity 89.3%; Pred. No. 3.6e-42;  
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYSGSHRA 60  
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYLSGNRA 60

QY 61 SGVPDRFSGVSGTDFTLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIK 112  
Db 61 SGVPDRFSGVSGTDFTLKISRVEADGVVYCMQGLQTPQTFGQGTKEIK 112

RESULT 3  
US-08-331-397B-49  
; Sequence 49, Application US/08331397B  
; Patent No. 5981726  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Benhar, Itai  
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331.397B  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-136120US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..112  
; OTHER INFORMATION: /note= "Human IgM antibody GM607  
; OTHER INFORMATION: Variable Light chain (V-L)"  
US-08-331-397B-49

Query Match 88.2%; Score 522; DB 2; Length 112;  
Best Local Similarity 89.3%; Pred. No. 3.6e-42;  
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYSGSHRA 60  
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLIIYLSGNRA 60

QY 61 SGVPDRFSGVSGTDFTLKISRVEADGVVYCMQGLQSPFTFGPGTKVDIK 112  
Db 61 SGVPDRFSGVSGTDFTLKISRVEADGVVYCMQGLQTPQTFGQGTKEIK 112



US-09-025-769B-178  
Sequence 178, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995

```

; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-178
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Query Match 86.1%; Score 510; DB 4; Length 281;
Best Local Similarity 86.7%; Pred. No. 1.3e-40;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Db 166 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSRA 225
Qy 61 SGVPDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 113
Db 226 SGVPDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 278

RESULT 9
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match 85.3%; Score 505; DB 4; Length 112;
Best Local Similarity 87.3%; Pred. No. 1.4e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 4 LTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRAGV 63
Db 3 LTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRAGV 62
Qy 64 PDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 113
Db 63 PDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 112

RESULT 10
US-08-082-623-4
; Sequence 4, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

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; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SDZ MSL 109"
US-08-082-623-4

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Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSRA 60
Qy 61 SGVPDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 113
Db 61 SGVPDRFSGVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGGKVDIKR 113

RESULT 11
US-08-478-039-88
; Sequence 88, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
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US-08-478-039-88
;
Query Match 84.6%; Score 501; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 3.4e-40;
Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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Db 1 DIVMTQSLPVPVTPGPASISCRSSQSLVHSNGNTYLNWYLQKPGQSPQLLIYKVSNR 60
;
Qy 61 SGVPDRFSGSGGTDFTLRIISRVEAEDGVVYCMQGLQSPFTFGPTKVDIK 112
Db 61 SGVPDRFSGSGGTDFTLRIISRVEAEDGVVYCMQALQSPYTFGGTKNEIK 112
;
RESULT 12
US-08-476-349A-88
; Sequence 88, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabill
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
;
US-08-476-349A-88
;
Query Match 84.6%; Score 501; DB 1; Length 112;
Best Local Similarity 85.7%; Pred. No. 3.4e-40;
Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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Qy 1 EIVLTQSLPVPVTPGPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSLPVPVTPGPASISCRSSQSLVHSNGNTYLNWYLQKPGQSPQLLIYKVSNR 60
;
Qy 61 SGVPDRFSGSGGTDFTLRIISRVEAEDGVVYCMQGLQSPFTFGPTKVDIK 112
Db 61 SGVPDRFSGSGGTDFTLRIISRVEAEDGVVYCMQALQSPYTFGGTKNEIK 112
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RESULT 13
US-08-053-171-16
; Sequence 16, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-10

Query Match      81.8%; Score 484.5; DB 1; Length 113;
Best Local Similarity 84.1%; Pred. No. 1.2e-38;
Matches 95; Conservative 10; Mismatches 7; Indels 1; Gaps

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Db    1 DIVMTQTPLSLVTPGEPAISCRSSSLDSDDGNTYLDWYLQKPGSQPLLIIYTLSYR 60
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY   60 ASGVPDFRGSGSGTGFTLIKISRVEADVGYYICMGLOSPETFGPKTKVDIK 112
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    61 ASGVPDFRGSGSGTGFTLIKISRVEADVGYYICMORIEPFFTFGGCTKVEIK 113
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RESULT 15
US-08-331-398A-50
Sequence 50. Application US/08331398A
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; STRANDEDNESS:
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; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 Variable Light
; chain (V-L) (HumB3V-L)"
US-08-331-398A-50

Query Match      81.8%; Score 484; DB 1; Length 112;
Best Local Similarity 81.2%; Pred. No. 1.3e-39;
Matches 91; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

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Qy 61 SGVPDRFSGSVGTDFTLRISVEAEDGVVYCMGLOSPETFGPTKVDIK 112
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Job time : 5.61224 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:10:35 ; Search time 44.537 Seconds  
(without alignments)  
893.051 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592

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Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 26: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	592	100.0	381	19	US-09-538-913-5
5	592	100.0	381	22	US-09-822-698A-5
6	534	90.2	262	1	PCT-US01-19110-2081
7	534	90.2	262	22	US-09-880-748-2081

8	532	89.9	113	18	US-09-490-070-15	Sequence 15, Appl
9	524	88.5	112	11	US-08-700-737-8	Sequence 8, Appl
10	524	88.5	112	16	US-09-254-180B-9	Sequence 9, Appl
11	523.5	88.4	114	18	US-09-430-048-19	Sequence 19, Appl
12	523.5	88.4	131	18	US-09-430-048-25	Sequence 25, Appl
13	522	88.2	112	7	US-08-331-396-49	Sequence 49, Appl
14	522	88.2	112	7	US-08-331-396A-49	Sequence 49, Appl
15	522	88.2	112	7	US-08-331-396C-49	Sequence 49, Appl
16	522	88.2	112	7	US-08-331-397-49	Sequence 49, Appl
17	522	88.2	112	7	US-08-331-398-49	Sequence 49, Appl
18	522	88.2	112	11	US-08-759-804-49	Sequence 49, Appl
19	518.5	87.6	112	18	US-09-430-048-20	Sequence 20, Appl
20	517.5	87.4	248	19	US-09-517-225E-6	Sequence 6, Appl
21	515	87.0	219	23	US-09-972-656-104	Sequence 104, App
22	514	86.8	125	1	PCT-US02-02303-50	Sequence 50, Appl
23	513	86.7	146	22	US-09-834-366-18022	Sequence 18022, A
24	513	86.7	146	26	US-09-197-873-18022	Sequence 18022, A
25	513	86.7	239	23	US-09-924-340-8	Sequence 8, Appl
26	513	86.7	239	23	US-09-994-590-8	Sequence 8, Appl
27	513	86.7	239	24	US-10-000-489-8	Sequence 8, Appl
28	513	86.7	239	24	US-10-000-489-8	Sequence 8, Appl
29	513	86.7	239	26	US-60-305-456-8	Sequence 8, Appl
30	513	86.7	239	26	US-60-305-456-8	Sequence 8, Appl
31	510	86.1	114	18	US-09-490-070-29	Sequence 29, Appl
32	510	86.1	114	18	US-09-490-070-45	Sequence 45, Appl
33	510	86.1	281	18	US-09-490-070-178	Sequence 178, App
34	505	85.3	112	22	US-09-848-798-30	Sequence 30, Appl
35	505	85.3	112	22	US-09-848-798A-30	Sequence 30, Appl
36	502	84.8	113	1	PCT-US94-01068-4	Sequence 4, Appl
37	501	84.6	113	23	US-09-900-135-17	Sequence 17, Appl
38	501	84.6	113	24	US-10-023-809-17	Sequence 17, Appl
39	495	83.6	142	22	US-09-834-366-13450	Sequence 13450, A
40	495	83.6	142	26	US-09-197-873-13450	Sequence 13450, A
41	486.5	82.2	260	1	PCT-US01-19110-1039	Sequence 1039, Ap
42	486.5	82.2	260	22	US-09-880-748-1039	Sequence 1039, Ap
43	486	82.1	219	23	US-09-972-656-94	Sequence 94, Appl
44	484	81.8	112	7	US-08-331-396-50	Sequence 50, Appl
45	484	81.8	112	7	US-08-331-396A-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-09-538-913-1  
; Sequence 1, Application US/09538913  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderixx, Paula  
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE  
; FILE REFERENCE: seqlist DYX-15  
; CURRENT APPLICATION NUMBER: US/09/538.913  
; CURRENT FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-538-913-1

Query Match	100.0%	Score 592;	DB 19;	Length 113;
Best Local Similarity	100.0%	Pred. No. 1e-50;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSPVLPVTPGPASISCRSSQLHSNGTYLDWYLPKPGSPOLLVYSGSHRA	60	
Db	1	EIVLTQSPVLPVTPGPASISCRSSQLHSNGTYLDWYLPKPGSPOLLVYSGSHRA	60	
QY	61	SGVPDRFSGVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTKVDIKR	113	
Db	61	SGVPDRFSGVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTKVDIKR	113	

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RESULT 2
US-09-822-698A-1
; Sequence 1, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1
Query Match 100.0%; Score 592; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 8.1e-50;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
RESULT 3
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24
Query Match 100.0%; Score 592; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
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RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
; OTHER INFORMATION: protein
US-09-538-913-5
Query Match 100.0%; Score 592; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 239
RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPHI-IL-2
US-09-822-698A-5
Query Match 100.0%; Score 592; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMGLOSPFTFGPTGKVDIKR 239
RESULT 6
PCT-US01-19110-2081
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; Sequence 2081, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2081

Query Match      90.2%; Score 534; DB 1; Length 262;
Best Local Similarity 90.3%; Pred. No. 1e-43;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 150 EIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGNRA 209

QY 61 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 210 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQALQPTLTFGGGKTKVEIKR 262

RESULT 7
US-09-880-748-2081
US-09-880-748-2081
; Sequence 2081, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match      90.2%; Score 534; DB 22; Length 262;
Best Local Similarity 90.3%; Pred. No. 1e-43;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 150 EIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGNRA 209
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QY 61 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 210 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQALQPTLTFGGGKTKVEIKR 262

RESULT 8
US-09-490-070-15
US-09-490-070-15
; Sequence 15, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,769
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070-15

Query Match      89.9%; Score 532; DB 18; Length 113;
Best Local Similarity 88.5%; Pred. No. 6e-44;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 1 DIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGNRA 60

QY 61 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSGSVSGTDTFLTKISRVEAEDGVVYCMQALQPTLTFGGGKTKLEIKR 113

RESULT 9
US-08-700-737-8
US-08-700-737-8
; Sequence 8, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Farran
; APPLICANT: Newman, Walter
```

APPLICANT: Saldanha, Jos  
APPLICANT: Bendig, Mary M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7  
TITLE OF INVENTION: INTEGRIN  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,737  
FILING DATE: 15-AUG-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS95-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-700-737-8

Query Match 88.5%; Score 524; DB 11; Length 112;  
Best Local Similarity 89.3%; Pred. No. 3.6e-43;  
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYLSNRA 60  
Qy 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIK 112  
Db 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIK 112

RESULT 10  
US-09-254-1808-9  
Sequence 9, Application US/092541808  
GENERAL INFORMATION:  
APPLICANT: Sumitomo Electric Industries  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTING SPECIFICALLY WITH Fas  
TITLE OF INVENTION: LIGAND OR ACTIVE FRAGMENTS THEREOF, AND REGION INDUCING  
TITLE OF INVENTION: APOPTOSIS ORIGINATING IN Fas LIGAND  
FILE REFERENCE: Attorney Docket 50006-055  
CURRENT APPLICATION NUMBER: US/09/254.1808  
CURRENT FILING DATE: 1995-04-15  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Human  
US-09-254-1808-9

Query Match 88.5%; Score 524; DB 16; Length 112;  
Best Local Similarity 87.5%; Pred. No. 3.6e-43;  
Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60

Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYLSNRA 60  
Qy 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIK 112  
Db 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIK 112  
RESULT 11  
US-09-430-048-19  
Sequence 19, Application US/09430048  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L.  
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions  
TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha  
FILE REFERENCE: 011.00231  
CURRENT APPLICATION NUMBER: US/09/430,048  
CURRENT FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 60/106,275  
PRIOR FILING DATE: 1998-10-30  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-430-048-19

Query Match 88.4%; Score 523.5; DB 18; Length 114;  
Best Local Similarity 87.7%; Pred. No. 4.1e-43;  
Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60  
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYLSNRA 60  
Qy 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIKR 113  
Db 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIKR 114

RESULT 12  
US-09-430-048-25  
Sequence 25, Application US/09430048  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L.  
TITLE OF INVENTION: Variable Heavy Chain and Variable Light Chain Regions  
TITLE OF INVENTION: Of Antibodies to Human Platelet Glycoprotein Ib Alpha  
FILE REFERENCE: 011.00231  
CURRENT APPLICATION NUMBER: US/09/430,048  
CURRENT FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 60/106,275  
PRIOR FILING DATE: 1998-10-30  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-430-048-25

Query Match 88.4%; Score 523.5; DB 18; Length 131;  
Best Local Similarity 87.7%; Pred. No. 4.8e-43;  
Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

Qy 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60  
Db 18 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYLSNRA 77  
Qy 61 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIKR 113  
Db 78 SGVPDRFSGSGTDTFLTRISRVEADGVGYVCMQALQPTFTFGQGTKEIKR 131

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RESULT 13
US-08-331-396-49
; Sequence 49, Application US/08331396
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Byungkook
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-08-331-396-49

Query Match      88.28; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112

QY 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112

RESULT 14
US-08-331-396A-49
; Sequence 49, Application US/08331396A
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira H.

```

```

; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL
; OTHER INFORMATION: region"
US-08-331-396A-49

Query Match      88.2%; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSGSGTDFTLRISRVEAEDVGVYCMQGLQSPFTFGPGTKVDIK 112

RESULT 15
US-08-331-396C-49
; Sequence 49, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,

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; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-396C-49

Query Match 88.2%; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSLPLVPTGEPASISCRSSQSLHNSGYLYLDWYLOKPGOSPQLIYSGSHRA 60
Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYLYLDWYLOKPGOSPQLIYLSNRA 60

Qy 61 SGVPDRFSGSVGCTDFTLRISVEAEDVGYYCMQGLQSPFTFGPTGKVDIK 112
Db 61 SGVPDRFSGSGGTDFTLRISVEAEDVGYYCMQGLQTPQTGQGTKEIK 112

Search completed: October 9, 2002, 19:19:26
Job time : 45.537 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 : Search time 14.9898 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698a-1

Perfect score: 592

Sequence: 1 EIVLTQSPSLPVTGPSPAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_New:\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
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- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	540	91.2	114	5 US-09-791-537-86326
2	533	90.0	136	5 US-09-791-537-71827
3	533	90.0	137	5 US-09-791-537-56427
4	531	89.7	114	5 US-09-791-537-86001
5	529	89.4	116	5 US-09-791-537-43479
6	529	89.4	117	5 US-09-791-537-48291
7	529	89.4	118	5 US-09-791-537-129360
8	529	89.4	135	5 US-09-791-537-12279
9	528	89.4	135	5 US-09-791-537-123428
10	528	89.2	112	5 US-09-791-537-21285
11	527	89.0	114	5 US-09-791-537-137519
12	527	89.0	117	5 US-09-791-537-107503
13	526	88.9	113	5 US-09-791-537-59499
14	524	88.5	125	6 US-10-010-942B-6
15	524	88.5	132	5 US-09-791-537-78289
16	523	88.3	118	5 US-09-791-537-54839
17	522	88.2	112	5 US-09-791-537-21281
18	522	88.2	112	5 US-09-791-537-110202
19	522	88.0	125	5 US-09-791-537-26052
20	521	88.0	112	5 US-09-791-537-34978
21	521	88.0	113	5 US-09-791-537-64225
22	520.5	87.9	115	5 US-09-791-537-137518
23	520	87.8	112	5 US-09-791-537-10195
24	516	87.2	113	5 US-09-791-537-106796
25	513	86.7	239	5 US-09-992-600A-8
26	511.5	86.4	114	5 US-09-791-537-64706

27	511	86.3	109	5	US-09-791-537-106940	Sequence 106940,
28	510	86.1	113	1	PCT-US02-12202-9	Sequence 9, Appli
29	510	86.1	113	6	US-10-025-687-9	Sequence 9, Appli
30	510	86.1	113	6	US-10-125-687-9	Sequence 9, Appli
31	506	85.5	114	6	US-10-041-860-322	Sequence 322, App
32	505	85.3	110	5	US-09-791-537-62920	Sequence 62920, A
33	505	85.3	121	5	US-09-791-537-26091	Sequence 26091, A
34	504.5	85.2	114	5	US-09-791-537-122965	Sequence 122965,
35	504	85.1	112	5	US-09-791-537-85986	Sequence 85986, A
36	503	85.0	138	1	PCT-US02-09694-52	Sequence 32, Appl
37	500.5	84.5	111	6	US-10-041-860-16	Sequence 16, Appl
38	500.5	84.5	111	6	US-10-041-860-220	Sequence 220, App
39	500.5	84.5	111	6	US-10-041-860-254	Sequence 254, App
40	500.5	84.5	111	6	US-10-041-860-279	Sequence 279, App
41	500	84.5	111	5	US-09-791-537-138276	Sequence 138276,
42	499.5	84.4	113	6	US-10-041-860-30	Sequence 30, Appl
43	499.5	84.4	113	6	US-10-041-860-221	Sequence 221, App
44	499.5	84.4	113	6	US-10-041-860-255	Sequence 255, App
45	499	84.3	110	5	US-09-791-537-22324	Sequence 22324, A

## ALIGNMENTS

RESULT 1  
US-09-791-537-86326  
; Sequence 86326, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86326  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-86326

Query Match 91.2%; Score 540; DB 5; Length 114;  
Best Local Similarity 91.2%; Pred. No. 5.7e-34;  
Matches 103; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
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Db 1 DIVMTQSPSLPVTGPSPASISCRSSQSLHNSGYNYLDWYLNKQKQSPQLLIYGSNRA 60  
QY 61 SGVPDRSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 113  
Db 61 SGVPDRSGSVSGTDFTLRISRVEAEDVGYYCMQALQTLFTFGPTKVDIKR 113  
RESULT 2  
US-09-791-537-71827  
; Sequence 71827, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 71827  
; LENGTH: 136



Db 65 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 117

## RESULT 7

US-09-791-537-129360

; Sequence 129360, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 129360

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-129360

Query Match 89.4%; Score 529; DB 5; Length 118;

Best Local Similarity 89.4%; Pred. No. 4e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

## RESULT 8

US-09-791-537-12279

; Sequence 12279, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12279

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-12279

Query Match 89.4%; Score 529; DB 5; Length 135;

Best Local Similarity 89.4%; Pred. No. 4.5e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 14 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYLSNRA 73

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 74 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 126

## RESULT 9

US-09-791-537-123428

; Sequence 123428, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 123428  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-123428

Query Match 89.4%; Score 529; DB 5; Length 135;

Best Local Similarity 89.4%; Pred. No. 4.5e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 14 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYLSNRA 73

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 74 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 126

## RESULT 10

US-09-791-537-21285

; Sequence 21285, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 21285

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-21285

Query Match 89.2%; Score 528; DB 5; Length 112;

Best Local Similarity 89.3%; Pred. No. 4.6e-33;

Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYLSNRA 60

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 112

Db 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 112

## RESULT 11

US-09-791-537-137519

; Sequence 137519, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

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; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 137519
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-137519

Query Match      89.0%; Score 527; DB 5; Length 114;
Best Local Similarity 89.4%; Pred. No. 5.5e-33;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLRKPGQSPQLLIYLSNRA 60
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Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADGVVYCMQGLQSPETFGPGTKVDIKR 113
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Db 61 SGVPDRFSGSGGTDTFLKISRVEADGVVYCMQALQTPPTFGGKTKVEIKR 113
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RESULT 12
US-09-791-537-107503
; Sequence 107503, Application us/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107503
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-107503

Query Match      89.0%; Score 527; DB 5; Length 117;
Best Local Similarity 89.4%; Pred. No. 5.6e-33;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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   :||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLRKPGQSPQLLIYLSNRA 64
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Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADGVVYCMQGLQSPETFGPGTKVDIKR 113
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Db 65 SGVPDRFSGSGGTDTFLKISRVEADGVVYCMQGLQTPQTPTFGGKTKVEIKR 117
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RESULT 13
US-09-791-537-59499
; Sequence 59499, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59499
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-59499
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US-09-791-537-59499

Query Match      88.9%; Score 526; DB 5; Length 113;
Best Local Similarity 88.5%; Pred. No. 6.5e-33;
Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
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Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLRKPGQSPQLLIYLSYRA 60
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Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADGVVYCMQGLQSPETFGPGTKVDIKR 113
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Db 61 SGVPDRFSGSGGTDTFLKISRVEADGVVYCMQALQTPPTFGGKTKVEIKR 113
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RESULT 14
US-10-010-942B-6
; Sequence 6, Application US/10010942B
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurij
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(13)
US-10-010-942B-6

Query Match      88.5%; Score 524; DB 6; Length 125;
Best Local Similarity 89.3%; Pred. No. 1e-32;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
   :||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 14 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLRKPGQSPQLLIYLSNRA 73
   :||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADGVVYCMQGLQSPETFGPGTKVDIK 112
   ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 74 SGVPDRFSGSGGTDTFLKISRVEADGVVYCMQALQTPPTFGGKTKVEIK 125
   ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

RESULT 15
US-09-791-537-78289
; Sequence 78289, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78289
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-78289
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Query Match      88.5%; Score 524; DB 5; Length 132;
Best Local Similarity 89.3%; Pred. No. 1.1e-32;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHLSNGYNYLDWYLOKPGQSPQLLIYLSNRA 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEADVGYYCMQGLQSPFTFGPGTKVDIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVPDRFSGSVSGTDFTLIRISRVEADVGYYCMQALQIPQTFGQGTKEIK 132

```

Search completed: October 9, 2002, 19:21:22  
 Job time : 14.9898 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 6.05357 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592  
Sequence: 1 EIVLTQSPSLPVTGPGEAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : FIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	90.0	136	2 S40357	Ig kappa chain V-J
2	529	89.4	135	2 S40342	Ig kappa chain - h
3	528	89.2	112	2 S58207	Ig light chain V r
4	527	89.0	117	1 K2HUGM	Ig kappa chain pre
5	524	88.5	132	2 S26882	Ig kappa chain V r
6	522	88.2	112	2 S58206	Ig light chain V r
7	522	88.2	125	2 S40356	Ig kappa chain - h
8	507.5	85.7	126	2 S40339	Ig kappa chain - h
9	505	85.3	121	2 S40371	Ig kappa chain - h
10	500	84.5	113	1 K2HUTW	Ig kappa chain V-J
11	494	83.4	131	2 S40372	Ig kappa chain V-I
12	484	81.8	124	2 S03876	Ig kappa chain V-I
13	478.5	80.8	112	1 K2HUML	Ig kappa chain V-I
14	478	80.7	123	2 S40319	Ig kappa chain V r
15	473.5	80.0	130	2 S40321	Ig kappa chain - h
16	467.5	79.0	115	1 K2HUCM	Ig kappa chain V-I
17	467	78.9	100	2 S24681	Ig kappa chain - h
18	457	77.2	113	2 PL0203	anti-DNA autoantib
19	457	77.2	114	2 S40375	Ig kappa chain - h
20	455	76.9	113	1 K2HUPR	Ig kappa chain V-I
21	452.5	76.4	114	2 S40340	Ig kappa chain V-J
22	449	75.8	131	2 B39276	Ig light chain pre
23	447	75.5	142	2 S22902	Ig kappa chain V r
24	447	75.5	219	2 S52028	Ig kappa chain - m
25	446	75.3	133	2 S23230	Ig kappa chain pre
26	445.5	75.3	127	2 S40323	Ig kappa chain - h
27	445	75.2	114	2 A32967	Ig kappa chain V-I
28	445	75.2	133	2 S40324	Ig kappa chain V r
29	444	75.0	112	2 A31807	Ig kappa chain V r

30	444	75.0	131	2 B30577	Ig kappa chain pre
31	444	75.0	133	1 K2HURP	Ig kappa chain pre
32	444	75.0	219	2 PC4203	Ig kappa chain (no
33	443	74.8	112	2 I26317	Ig kappa chain V r
34	443	74.8	118	2 PT0359	Ig kappa chain V r
35	443	74.8	197	2 S29593	Ig kappa chain (WM
36	442.5	74.7	126	2 S40341	Ig kappa chain - h
37	442	74.7	112	2 G26317	Ig kappa chain V r
38	442	74.7	112	2 S38719	Ig light chain V r
39	442	74.7	115	2 S38715	Ig kappa chain V r
40	442	74.7	122	2 S40338	Ig kappa chain - h
41	441	74.5	112	2 A26317	Ig kappa chain V r
42	441	74.5	112	2 F27887	Ig kappa chain V r
43	441	74.5	112	2 F26317	Ig kappa chain V r
44	441	74.5	113	2 B41940	Ig light chain V r
45	441	74.5	126	2 S40312	Ig kappa chain - h

## ALIGNMENTS

### RESULT 1

S40357  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40357  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40357  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-136 <KLE>  
A:Cross-references: EMBL:X72467  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 533; DB 2; Length 136;  
Best Local Similarity 89.4%; Pred. No. 6.8e-42;  
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY	1	EIVLTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGSHRA	60
Db	21	DIVMTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGOSPQLLIYSGNRA	80
QY	61	SCVPDRFSGSVSGTDFTLRISRVEADVGYYICMQGLQSPFTFGPTKVDIKR	113
Db	81	SCVPDRFSGSVSGTDFTLRISRVEADVGYYICMQALQTPWTFGGTKVETKR	133

### RESULT 2

S40342  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40342  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40342  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-135 <KLE>  
A:Cross-references: EMBL:X72452; NID:9441372; PID:9441373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 529; DB 2; Length 135;

Best Local Similarity 89.4%; Pred. No. 1.6e-41;  
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLKPKGSPQLLIYSGSRA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 14 DIVMTQSPLSPVTPGEPASISCRSSQSLHNSGYNYLDWYLKPKGSPQLLIYLSNRA 73

QY 61 SGVPDRFSGSVSGTDFTLRISRVEADGVVYCMQGLOSPFTFGPTGKTVDIKR 113  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 74 SGVPDRFSGSGTGDTFLKISRVEADGVVYCMQALQTPTFGGTKEIKR 126

RESULT 3  
S58207  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
R:Accession: S58207  
C:Wellshof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; DoebeI, S.; Breittling,  
submitted to the EMBL Data Library, July 1995  
A:Description: Characterization of heavy and light chain immunoglobulin variable region  
A:Reference number: S58206  
A:Accession: S58207  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <RES>  
C:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMX>

Query Match 89.2%; Score 528; DB 2; Length 112;  
Best Local Similarity 89.3%; Pred. No. 1.6e-41;  
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLKPKGSPQLLIYSGSRA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 DIVMTQSPLSPVTPGEPASISCRSSQSLHNSGYNYLDWYLKPKGSPQLLIYLSNRA 60

QY 61 SGVPDRFSGSVSGTDFTLRISRVEADGVVYCMQGLOSPFTFGPTGKTVDIK 112  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 SGVPDRFSGSGTGDTFLKISRVEADGVVYCMQALQTPTFGGTKEIK 112

RESULT 4  
K2HUGM  
Ig kappa chain precursor V-II region (GM607) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Jul-1999  
C:Accession: A01889; B24452  
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.  
Nature 309, 73-76, 1984  
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.  
A:Reference number: A01889; MUID:84191506  
A:Accession: A01889  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLO>  
A>Note: the sequence was determined from the differentiated gene  
C:Genetics:  
A:Gene: GDB:IGKV2  
A:Cross-references: GDB:I36265  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F:20-99/Domain: immunoglobulin homology <IMX>  
F:27-97/Disulfide bonds: #status predicted

Query Match 89.0%; Score 527; DB 1; Length 117;  
Best Local Similarity 89.4%; Pred. No. 2e-41;



```
|||||
Db 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIK 112

RESULT 7
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Accession: S40356
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 522; DB 2; Length 125;
Best Local Similarity 88.5%; Pred. No. 6.3e-41;
Matches 100; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||
Db 10 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYGSNRA 69
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113
|||||
Db 70 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 122

RESULT 8
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Accession: S40339
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 507.5; DB 2; Length 126;
Best Local Similarity 87.5%; Pred. No. 1.3e-39;
Matches 98; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||
Db 16 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYGSNRA 75
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 112
|||||
Db 76 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 126

RESULT 9
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
```

```
C:Accession: S40371
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40371
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 505; DB 2; Length 121;
Best Local Similarity 87.3%; Pred. No. 2.2e-39;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRAGV 63
:|||||
Db 1 MTQSPSLSPVTPGEPASISCRSSQSLYSTGYNDWYLOKPGKSPQLLIYLSKRAGV 60
:|||||

QY 64 PDRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113
|||||
Db 61 PDRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 110

RESULT 10
Ig kappa chain V-II region (Tew) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
A:Accession: A90370; A92764; A01888
R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary am
A:Reference number: A90370; MUID:74148480
A:Contents: Bence Jones protein Tew
A:Accession: A90370
A:Molecule type: protein
A:Residues: 1-113 <PUT>
A:Note: This protein was isolated from the urine of a patient with plasma cell dyscra
A:Note: the C region of this chain has the Inv (1,2) marker
R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glennier, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient
A:Reference number: A92764; MUID:73166638
A:Contents: amyloid protein Tew
A:Accession: A92764
A:Molecule type: protein
A:Residues: 1-27 <TER>
A:Note: the major amyloid protein appears to be identical with the Bence Jones protei
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 84.5%; Score 500; DB 1; Length 113;
Best Local Similarity 82.3%; Pred. No. 5.8e-39;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
:|||||
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGDFYLNWYLOKPGQSP2LLIYALSNA 60
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113
|||||
```



A:Accession: S40321  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-130 <KLE>  
A:Cross-references: EMBL:X72431  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:31-111/Domain: Immunoglobulin homology <IMM>

```

Query Match      80.0%: Score 473.5: DB 2: Length 130;
Best Local Similarity 80.7%: Pred. No. 1.8e-36;
Matches 92: Conservative 13: Mismatches 8: Indels 1: Gaps 1:

Qy 1 EIVLTGSLPLVPTGEPASISCRSSOSLLHS-NGYTYLDWYLKQPGSQPLLIVSGSHR 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 16 DIVMTGTLPLVPTGEPASISCRSSOSLLSDSDGNITLDWYLKQPGSQPLLIVTLYSR 75
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

Qy 60 ASGVPPDRFGSGVSGDFTLRISRVAEADGVYYVCMQGLSQSPFTFGTGVKDIKR 113
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 76 ASGVPPDRFGSGSGTAFTLKISRVAEADGVLYVCMQRIEPPYFTGGTKLEIKR 129
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

Search completed: October 9, 2002, 19:13:19  
Job time : 7.05357 secs





QY	61	SGVPPDRFSGSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR	113
Db	65	SGVPPDRFSGSGTDFTLIRSRVEADGVVYCMQGLQTPQTGGQTRVEIKR	117
RESULT 2			
ID	KV2D_HUMAN	STANDARD;	PRT; 113 AA.
AC	P01617;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region TEW.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
SEQUENCE (BENCE-JONES PROTEIN TEW).			
RX	MEDLINE=74148480; PubMed=4596149;		
RA	Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;		
RT	"Amino acid sequence of a kappa Bence Jones protein from a case of		
RT	primary amyloidosis."		
RL	Biochemistry 12:3763-3780(1973).		
RN	[2]		
SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).			
RX	MEDLINE=73166638; PubMed=4700495;		
RA	Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,		
RA	Glennner G.G.;		
RT	"Structural identity of Bence Jones and amyloid fibril proteins in a		
RT	patient with plasma cell dyscrasia and amyloidosis."		
RL	J. Clin. Invest. 52:1276-1281(1973).		
CC	-1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL		
CC	WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.		
CC	-1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A		
CC	PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.		
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)		
CC	MARKER.		
DR	PIR; A01888; K2HUTW.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
KW	Immunoglobulin V region; Bence-Jones protein; Amyloid.		
FT	DOMAIN 1 23 FRAMEWORK-1.		
FT	DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.		
FT	DOMAIN 40 54 FRAMEWORK-2.		
FT	DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.		
FT	DOMAIN 62 93 FRAMEWORK-3.		
FT	DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.		
FT	DOMAIN 103 112 FRAMEWORK-4.		
FT	DISULFID 23 93 BY SIMILARITY.		
FT	NON_TER 113 113		
SQ	SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;		
Query Match 84.5%; Score 500; DB 1; Length 113;			
Best Local Similarity 82.3%; Pred. No. 1e-43;			
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;			
QY	1	EIVTQSPSLPVTGPGEPASISCRSSQLHNSGYTLVDWYLOKPGSPOLLIIYSGSHRA	60
Db	1	DIVMTQSPSLPVTGPGEPASISCRSSQLHNSGDFLNNWYLOKPGSPZLLIYALSNRA	60
RESULT 3			
ID	KV2C_HUMAN	STANDARD;	PRT; 112 AA.
AC	P01616;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region Cum.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
SEQUENCE.			
RX	MEDLINE=68242259; PubMed=5586923;		
RA	Hiltschmann N.;		
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-		
RT	type).";		
RL	Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).		
RN	[2]		
RP	REVIEWS TO 50; 52; 96 AND 97.		
RX	MEDLINE=70063440; PubMed=4188189;		
RA	Hiltschmann N.;		
RT	"Molecular basis of antibody formation.";		
RL	Naturwissenschaften 56:195-205(1969).		
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.		
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.		

```
DR PIR: A01885; K2HUCM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin v region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 79.08; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 1.9e-40;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLVPTGPEPASISCRSSQSLHLS-NGYTYLDWYLOKPGQSPQLLIYSGSHR 59
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 2 DIVMTQSLPLVPTGPEPASISCRSSQSLDSDGNTYLNWYLOKAGQSPQLLIYLSYR 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 60 ASGVPDFRSGSGVSGDTFLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 62 ASGVPDFRSGSGVSGDTFLIRSRVQAEADVGVYYCMQRLPIPTFGQGTKEIKR 115
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 5
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
   with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
   -!- MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
PIR: A01886; K2HURF.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 76.98; Score 455; DB 1; Length 113;
Best Local Similarity 74.38; Pred. No. 3.4e-39;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPTGPEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHR 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIVMTQSLPLVPTLGEPAISQCRSSQSLVYRBGTYLBNWYLOKPGQSPPELLIYLSYRD 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVSGDTFLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 SGVPDRFSGSGVSGDTFLIKITRVQAEADVGVYYCMQATZSPYTFGQGTKEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 6
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
   III.";
RT Nucleic Acids Res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
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   or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00020; CAA77315.1; -.
DR PIR: A01890; K2HURP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 122
FT DOMAIN 123 132
FT DISULFID 43 113
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 75.08; Score 444; DB 1; Length 133;
Best Local Similarity 75.2%; Pred. No. 5.3e-38;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSLPLVPTGPEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHR 60
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 21 DIVMTQSLPLVPTLGEPAISCRSSQSLVSDGNTYLNWYLOKPGQSPRLIYKVSNRD 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 SGVPDRFSGSVSGDTFLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 81 SGVPDRFSGSGVSGDTFLIKISRVAEADVGVYYCMQGTHTWSWTFGQGTKEIKR 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 7
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TRISU=Hybridoma;
RA MEDLINE=85128968; PubMed=6441768;
RX Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of c57Bl/6
RT origin: monoclonal antibodies 17529.1 and 22525.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 73.0%; Score 432; DB 1; Length 113;
Best Local Similarity 75.2%; Pred. No. 7.le-37; Indels 0; Gaps 0;
Matches 85; Conservative 10; Mismatches 18;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQAVSNPVTIGTASISCRSSKSLHNSGYTYLYWYLRKPGQSPQLLIYQMSNLA 60
QY 61 SGVPDRFSGSVSGTDTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDTLIRSRVEADGVVYCAHNLPLPYTGGGKLEIKR 113

RESULT 8
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 5.7e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQATPSALVTPGVSISCRSSKSLHNSGYTYLYWYLRKPGQSPQLLIYRMSNLA 60
QY 61 SGVPDRFSGSVSGTDTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDTLIRSRVEADGVVYCMQQRQREYPYTFGGGKLEIKR 113
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FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 72.5%; Score 429; DB 1; Length 113;
Best Local Similarity 72.6%; Pred. No. 1.4e-36;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQTPLESLPVSLGDAQSISCRSSQSLHNSGYTYLYWYLRKAGQSPKLLIYKYSNRF 60
QY 61 SGVPDRFSGSVSGTDTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSGSGTDTLIRSRVEADGLIYFCSQTTTHVPPTFGGKLEIKR 113

RESULT 9
KV2F_MOUSE STANDARD; PRT; 113 AA.
ID KV2F_MOUSE
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 5.7e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
DB 1 DIVMTQATPSALVTPGVSISCRSSKSLHNSGYTYLYWYLRKPGQSPQLLIYRMSNLA 60
QY 61 SGVPDRFSGSVSGTDTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDTLIRSRVEADGVVYCMQQRQREYPYTFGGGKLEIKR 113
```



CC CHAINS.

CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF

CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

CC PIR; A01907; K2DGGM.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig: 1.

DR SMART; SM00406; IGV: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 88

FT NON\_TER 108 108

FT SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 66.6%; Score 394.5; DB 1; Length 108;

Best Local Similarity 69.0%; Pred. No. 4e-33;

Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPAISCRSSOSLLHSNGTYTLDWYLOKQSQPOLLIYSGSHRA 60

DB 1 DIVWTQTPLSVSGEPAISCRSSQSNL-----DYLNWYLOKAGQSPRLPEQDSQRA 55

QY 61 SGVPDRFSGSVSGDFTFLRISRVAEDVGVYCMQGLQSPFTGPGTKVDIKR 113

DB 56 SGVPDRFSGSGSDFTFLRIGRVEADAGIYCMQRSFYPTGFGTRLEVR 108

RESULT 12

KV2C\_MOUSE

ID KV2C\_MOUSE STANDARD; PRT; 113 AA.

AC P01628;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region MOPC 511.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=81052016; PubMed=6776396;

RA Appella E.;

RT "Amino acid sequence of the light chain variable region of M511, a

RT phosphorylcholine-binding murine myeloma protein.";

RL Mol. Immunol. 17:711-718(1980).

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT

CC BINDS PHOSPHORYLCHOLINE.

CC PIR; A01910; KVM551.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig: 1.

DR SMART; SM00406; IGV: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT DOMAIN 24 39

FT DOMAIN 40 54

FT DOMAIN 55 61

FT DOMAIN 62 93

FT DOMAIN 94 102

FT DOMAIN 103 112

FT DISULFID 23 93

FT NON\_TER 113 113

FT SEQUENCE 113 AA; 12496 MW; EEF0DC4DA2BD3450 CRC64;

Query Match 66.6%; Score 394; DB 1; Length 113;

Best Local Similarity 69.0%; Pred. No. 4.7e-33;

```
Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLTPEGPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIVITQDELSPVTSGESVYSICRSKSLLYKDGKTYLNWFLQPGQSPQLLIYLMSTRA 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SGVPDRFSGSVGTDFTLRISRVAEADVGVYCMGGLQSPFTFGGTVKVDIKR 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SGVSDRFSGSGVTDFTLRISRVKAEADVGVYCCQLVEYPLTFGAGTKLELKR 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
KV2A_MOUSE STANDARD; PRT; 112 AA.
ID KV2A_MOUSE
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein."
RL Biochemistry 17:2703-2707(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CHAIN HAS ALSO BEEN DETERMINED.
CC PIR; A01908; KVM516.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD640B9726 CRC64;

Query Match 65.4%; Score 387; DB 1; Length 112;
Best Local Similarity 68.8%; Pred. No. 2.4e-32;
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLTPEGPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIVITQDELSPVTSGESVYSICRSKSLLYKDGKTYLNWFLQRPQSPQLLIYLMSTRA 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SGVPDRFSGSVGTDFTLRISRVAEADVGVYCMGGLQSPFTFGGTVKVDIK 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SGVSDRFSGSGVTDFTLRISRVKAEADVGVYCCQLVEYPLTFGAGTKLELKR 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; P18135;
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; P18135;
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 62.5%; Score 370; DB 1; Length 129;
Best Local Similarity 66.4%; Pred. No. 1.4e-30;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;
QY 1 EIVLTQSPVLTPEGPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 EIVLTQSPGTLSPGERATLSCRASQSVSS---YLAAYQKPGQAPRLLIYGASSRA 76
:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 SGVPDRFSGSVGTDFTLRISRVAEADVGVYCMGGLQSPFTFGGTVKVDIKR 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 TGIPDRFSGSGVTDFTLRISRVKAEADVGVYCCQLVEYPLTFGAGTKLELKR 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
KV3M_HUMAN STANDARD; PRT; 129 AA.
ID KV3M_HUMAN
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; P18136;
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
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DR Pfam: PF00047; ig: 1.
DR SMART: SM00406; igv: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BE74D6 CRC64;

Query Match 62.3%; Score 369; DB 1; Length 129;
Best Local Similarity 65.5%; Pred. No. 1.8e-30;
Matches 74; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPPLSLPVTGPGEPAISICRSQSLHSHNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
Db 21 EIVLTQSPGTLSPGGERATLSCRASQSVSS---YLAWYQKQKPGQAPRLLIYGASSRA 76
QY 61 SGVPDFRFSVGSGTDFTLRIISRVEREDGVYVCMQGLQSPFTFGPTKVDIKR 113
Db 77 TGIPDRFSGSGSGTDFTLTIISRLKLEPDAFYVYCQYQYGGSPWTFGGQTKVEIKR 129

Search completed: October 9, 2002, 19:11:04
Job time : 4.45918 secs
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:05:30 ; Search time 9.65689 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698a-1  
Perfect score: 592  
Sequence: 1 EIVLTQSPLSLPVTGPAPAS.....MGLQSPFTFGTKVDIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222.

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457	77.2	238	11 Q99M37	Q99M37 mus musculus
2	428.5	72.4	114	4 Q9UL80	Q9UL80 homo sapien
3	406	68.6	104	11 Q9UL82	Q9UL82 mus musculus
4	373	63.0	109	4 Q9UL78	Q9UL78 homo sapien
5	369	62.3	109	4 Q9UL86	Q9UL86 homo sapien
6	351.5	59.4	108	4 Q9UL83	Q9UL83 homo sapien
7	340.5	57.5	111	11 Q920E9	Q920E9 mus musculus
8	325.5	55.0	107	11 Q9ER29	Q9ER29 mus musculus
9	322	54.4	107	4 Q9UL81	Q9UL81 homo sapien
10	322	54.4	109	4 Q9UL85	Q9UL85 homo sapien
11	316.5	53.5	108	4 Q9UL77	Q9UL77 homo sapien
12	313	52.9	106	5 Q9UL10	Q9UL10 schistosoma
13	309.5	52.3	108	4 Q9UL79	Q9UL79 homo sapien
14	308	52.0	107	4 Q96SA9	Q96SA9 homo sapien
15	306.5	51.8	108	4 Q9UL70	Q9UL70 homo sapien
16	301.5	50.9	214	11 Q9RIAS	Q9RIAS mus musculus

17	296.5	50.1	298	11 Q9QYF0	Q9QYF0 mus musculus
18	293.5	49.6	109	11 Q920E6	Q920E6 mus musculus
19	289.5	48.9	211	11 Q9IXL0	Q9IXL0 mus musculus
20	288.5	48.7	116	4 Q96PF6	Q96PF6 homo sapien
21	286	48.3	235	11 Q9IWI2	Q9IWI2 mus musculus
22	284.5	48.1	103	11 Q9JL80	Q9JL80 mus musculus
23	283.5	47.9	99	11 Q9JL74	Q9JL74 mus musculus
24	282.5	47.7	234	11 Q9LWF8	Q9LWF8 mus musculus
25	276.5	46.7	101	11 Q9JL78	Q9JL78 mus musculus
26	270.5	45.7	233	11 Q9LWS9	Q9LWS9 mus musculus
27	265.5	44.8	97	11 Q9UL76	Q9UL76 mus musculus
28	255.5	43.2	127	11 Q925S9	Q925S9 mus musculus
29	249.5	42.1	109	6 Q9N0W5	Q9N0W5 oryctolagus
30	240.5	40.6	107	11 Q9JL84	Q9JL84 mus musculus
31	223.5	37.8	236	4 Q96E61	Q96E61 homo sapien
32	223	37.7	108	4 Q96SB0	Q96SB0 homo sapien
33	222	37.5	241	11 Q921A6	Q921A6 mus musculus
34	213.5	36.1	107	4 Q9UL82	Q9UL82 homo sapien
35	211.5	35.7	218	11 Q925S1	Q925S1 mus musculus
36	202.5	34.2	112	4 Q96JDI	Q96JDI homo sapien
37	201	34.0	107	4 Q9NSD6	Q9NSD6 homo sapien
38	198	33.4	116	4 Q96JD0	Q96JD0 homo sapien
39	197	33.3	112	4 Q96JD2	Q96JD2 homo sapien
40	185	31.2	235	11 Q9NM11	Q9NM11 mus musculus
41	182.5	30.8	130	4 Q9NP29	Q9NP29 homo sapien
42	181	30.6	233	4 Q96I69	Q96I69 homo sapien
43	169	28.5	233	11 Q9IV32	Q9IV32 m adult mal
44	164	27.7	109	11 Q9ET13	Q9ET13 mus musculus
45	151.5	25.6	154	11 Q91XK2	Q91XK2 mus musculus

## ALIGNMENTS

RESULT 1  
Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37; 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOHETICAL 26.3 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS  
RC TISSUE.;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC02035; AAH02035.1; -;  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003600; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 1.  
DR SMART; SM00406; IG; 1.  
DR SMART; SM00410; IG; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein..  
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 77.2%; Score 457; DB 11; Length 238;  
Best Local Similarity 75.2%; Pred. No. 7.3e-44;  
Matches 85; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

Oy 1 EIVLTQSPLSLPVTGPAPASISCRSSQSLHLSNGYIYLDWYLOKPGQSPQLLIYSGSHRA 60

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Db      20 DVMYQTPUSLSEVSGDQASICRSSHOSIVHSNGNTYLEWYLKPGQSPKLIIYKVSNR 79
        :::::|::::|::: |:::|::::|:::|:::|::::|:::|:::|::::|:::|:::|:::|
Qy      61 SGVPDRFSGSVGSDFTFLIRISRVEADGVGYCMQGSLQSPTFGTKVDIKR 113
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 SGVPDRFSGSGSDFTTLKISRVEADLVGYVFCQGHVPTFGSKLEIKR 132
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
QJUL80
ID      QJUL80 PRELIMINARY; PRT; 114 AA.
AC      QJUL80;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-DSC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE      (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
        Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
        fetus";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      ENBL; AF035034; AAD56270.1; -.
DR      HSSP; P80362; IWTL.
DR      InterPro; IPRO00306; Ig_MHC.
DR      InterPro; IPRO03596; Ig_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 1
FT      FT 114
SQ      SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 72.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 4.9e-41;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps

Qy      61 EVILTQSPLSLPVTGEFAPASICRSSQSLLHNSGTYTLDWYLNKPGQSPQLIYCSHRA 60
Db      1 DVMYTQSPLSLPVTQRQFASICSRSQSPVSDGNTYLNWFQRPQSPRRLIYKVSNRD 60
        :::::|::::|::: |:::|::::|:::|:::|::::|:::|:::|::::|:::|:::|:::|
Qy      61 SGVPDRFSGSVGSDFTFLIRISRVEADGVGYCMQGSLQ-SPFTFGTKVDIKR 113
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 SGVPDRFSGSGSDFTTLKISRVEADGVGYCMQGTGTHWPPTFGCTKVEIKR 114
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
QJUL82
ID      QJUL82 PRELIMINARY; PRT; 104 AA.
AC      QJUL82;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-DSC-2001 (TREMBLrel. 19, Last annotation update)
DE      ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE      (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RX      STRAIN=BALB/C;
RC      MEDLINE=20448942; PubMed=10992488;
RA      Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT      "T-cell-dependent antibody response to the dominant epitope of
        streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
        with cardiac myosin.";

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Qy	1	EIVLTOSPUSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSOLLIIYSGSRA	60
Dd	1	EIVTOSTPATLSVSPGERATISCRASOS-VSSN---LAWYQOKPGQAPRLIIYCASTRA	55
Qy	61	SGVPDRFSGSVGGTDFTLRISRVEAEDGVYYCMOGQLSQSPFTFGPTGKTVDIKR	113
Dd	56	TGIPARFSGSGGTETTLTISSLQFEDFAVYYCOHYNNWFTEFGPTGKTVDIKR	108
RESULT 7			
ID	Q920E9	PRELIMINARY:	PRT; 111 AA.
AC	Q920E9;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	PTERIN-MIMICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ackin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;		
RT	"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed		
RT	In Mammalian Cells.";		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
FR	EMBL; AF307935; AAL09419.1; -.		
DR	NON_TER 1		
FT	NON_TER 111		
SQ	SEQUENCE 111 AA; 12046 MW; 1E46988AA6958526 CRC64;		
Query Match 57.5%; Score 340.5; DB 11; Length 111;			
Best Local Similarity 59.8%; Pred. No. 4.7e-31;			
Matches 67; Conservative 17; Mismatches 27; Indels 1; Gaps			
Qy	1	EIVLTOSPUSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSOLLIIYSGSRA	60
Dd	1	DIVLTOSPASLAVSGQRATISCRASKS-VSTSGTSMHWYQOKPGPPKLLIYLASNLE	59
Qy	61	SGVPDRFSGSVGGTDFTLRISRVEAEDGVYYCMOGQLSQSPFTFGPTGKTVDIK	112
Dd	60	SGVPARFSGSGGTDFTLNIHPVEEDAATYYCQHSRELPTYFGGTTKLEIK	111
RESULT 8			
ID	Q9ERZ9	PRELIMINARY:	PRT; 107 AA.
AC	Q9ERZ9;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DRC-2001 (TREMBLrel. 19, Last annotation update)		
DE	ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;		
RT	"Cloning and sequencing of the light chain fragment of variable regi-		
RT	genes of an anti-HTNF-a monoclonal antibody.";		
RL	J. Cell. Mol. Immunol. 12:21-26(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;		
RT	"Construction and sequencing of the single-chain antibody gene of a		
RT	human TNF-alpha specific monoclonal antibody.";		
RL	Ti 4 Chun I Ta Hueeh Hsueh Pao 19:373-376(1998).		
RN	[3]		
RP	SEQUENCE FROM N.A.		

Query Match 53.5%; Score 316.5; DB 4; Length 108;



```
Best Local Similarity 54.9%; Pred. No. 2.4e-28;
Matches 62; Conservative 18; Mismatches 28; Indels 5; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :|:||||| :|: :|:||||| :|: :|:||||| :|: :|:||||| :|: :|:||||| :|:
Db 1 DIQMTQSPFSSLSASVGRVITTCRASQSI-----SSYLNWYQKPGKAPNLLIYAASLQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 113
   ||||| ||||| ||||| || :|: ||| :|: ||| :|: ||| :|: ||| :|: |||
Db 56 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 108

RESULT 12
Q9U410 PRELIMINARY; PRT; 106 AA.
ID Q9U410;
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MONOCLONAL ANTI-IDIOPTIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 52.9%; Score 313; DB 5; Length 106;
Best Local Similarity 54.5%; Pred. No. 6e-28;
Matches 61; Conservative 18; Mismatches 27; Indels 6; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   |:||||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|: ||| :|:
Db 1 ENLTSQPAIMASFGKVTMTCSASSV-----SYVWYLOKPGSSPRLLIYDTSNLA 54

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 112
   ||||| ||||| ||| :|: ||||| ||| ||||| ||||| ||||| |||||
Db 55 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 106

RESULT 13
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79;
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
```

```
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 52.3%; Score 309.5; DB 4; Length 108;
Best Local Similarity 55.8%; Pred. No. 1.5e-27;
Matches 63; Conservative 15; Mismatches 30; Indels 5; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :|:||||| :|: :|:||||| :|: :|:||||| :|: :|:||||| :|:
Db 1 DIVMTQSPFSSLSASGTGDRVTISCRMSQSI-----SSYLNWYQKPGKAPPELLIYAASLTQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 113
   ||||| ||||| ||||| || :|: ||| :|: ||| :|: ||| :|: ||| :|: |||
Db 56 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 108

RESULT 14
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=97112075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 52.0%; Score 308; DB 4; Length 107;
Best Local Similarity 55.8%; Pred. No. 2.2e-27;
Matches 63; Conservative 17; Mismatches 27; Indels 6; Gaps 2;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
   :|:||||| :|: :|:||||| :|: :|:||||| :|: :|:||||| :|:
Db 1 DIQMTQSPFSSLSASVGRVITTCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 113
   ||||| ||||| ||||| || :|: ||| :|: ||| :|: ||| :|: ||| :|: |||
Db 56 SGVPDRFSGSVSGTDFTLIRSRVEAEDVGYYCMQGLQSPFTFGPTGKVDIKR 107

RESULT 15
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
```

```
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 51.8%; Score 306.5; DB 4; Length 108;
Best Local Similarity 55.8%; Pred. NO. 3.3e-27;
Matches 63; Conservative 17; Mismatches 28; Indels 5; Gaps 2;

QY 1 EIVLTQSPFLSLPVTCEPASISCRSSQSLLHSNGYVYLDWYLQKPGQSPOLLIIYSGSHRA 60
Db 1 DIQMTQSPSSLSASVGDVRVITTCRASQGI--SN---YLAWYQQKPKGVKPSLIYAASLTQ 55

QY 61 SGVPRFSGSVSGTDFTLRISRVEAEADVGVYCMQGLQSPFTFGPTKVDIKR 113
Db 56 SGVPSRFSGSGSGTDFTLTITSLQPEDVATYYCQKYNAPRTFGPTGKLEIKR 108
```

Search completed: October 9, 2002, 19:12:24  
Job time : 10.6569 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:12:30 ; Search time 48.3214 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
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14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
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17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	451	100.0	451	22	AAU07745 Human recombinant
2	343	76.1	461	22	AAU07745 Humanised monoclon
3	342	75.8	449	14	AA193339 Completely humanis
4	342	75.8	449	17	AAW49816 Amino acid sequenc
5	342	75.8	475	19	AA193353 Monoclonal antibod
6	342	75.8	581	22	AA1981972 Ganglioside GD2 sp
7	342	75.8	583	22	AA1983156 Ganglioside GM2 an
8	342	75.8	731	22	AA1983156 Humanised HMFPG-1 h
9	342	75.8	741	22	AAW52159 Humanised HMFPG-1 h
10	341	75.6	475	22	AA1933640 Amino acid sequenc
11	341	75.6	476	14	AA1931023 Antibody D heavy c

12	341	75.6	481	13	AA1924442	Sequence of antibo
13	341	75.6	729	22	AAW52158	Humanised HMFPG-1 h
14	341	75.6	739	22	AAW52161	Humanised HMFPG-1 h
15	340	75.4	730	22	AAW52157	Humanised HMFPG-1 h
16	340	75.4	740	22	AAW52160	Humanised HMFPG-1 h
17	340	75.4	961	21	AAW52187	Human gpi30-J-C-qa
18	338	74.9	371	10	AAW521918	Sequence of the li
19	336	74.5	465	22	AAW52228	Humanised 323/A3 (
20	336	74.5	467	13	AAW522758	Reshaped CD4 antib
21	336	74.5	467	13	AAW522759	Reshaped CD4 antib
22	336	74.5	470	13	AAW522757	Reshaped CAMPATH-1
23	335	74.3	461	14	AAW522162	Anti-HIV-1 recombi
24	335	74.3	464	22	AAW52232	Humanised 323/A3 (
25	335	74.3	475	13	AAW520057	Heavy chain of 3D6
26	335	74.3	476	20	AAW52464	Monoclonal antibod
27	334	74.1	582	22	AAW521987	Ganglioside GD3 sp
28	334	74.1	582	22	AAW521991	Ganglioside GD3 sp
29	333	73.8	473	22	AAW524469	Human type antihum
30	333	73.8	473	22	AAW524471	Human type antihum
31	333	73.8	473	22	AAW524473	Human type antihum
32	333	73.8	473	22	AAW524475	Human type antihum
33	330	73.2	330	22	AAW524071	Zcytor 10::Igg gam
34	330	73.2	351	14	AAW523685	Human kappa immuno
35	330	73.2	447	20	AAW521669	Human IgG1 chain C
36	330	73.2	452	20	AAW523021	Heavy chain sequen
37	330	73.2	534	13	AAW526531	Sequence of CD4-Ig
38	330	73.2	547	22	AAW52579	Human IL-20RA-Ig g
39	330	73.2	571	22	AAW524065	Human IL-20RA/immu
40	330	73.2	571	22	AAW525278	Human IL-20RA-Ig g
41	330	73.2	595	20	AAW526003	Anti-5T4 single ch
42	330	73.2	652	19	AAW524650	Heavy chain of hMA
43	330	73.2	690	21	AAW52195	Human IL-6R-alpha-
44	330	73.2	729	10	AAW523008	Sequence encoded b
45	330	73.2	729	21	AAW52168	CD4-Ig fusion prot

#### ALIGNMENTS

RESULT 1  
AAE12715  
ID AAE12715 standard; Protein; 451 AA.  
XX  
AC AAE12715;  
XX  
DT 04-JAN-2002 (first entry)  
XX  
DE Human recombinant immunoglobulin (Ig) heavy chain region.  
XX  
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;  
KW heavy chain region; cancer; breast; ovary; lung; bladder;  
KW cytostatic; therapy; immunoglobulin; Ig.  
XX  
OS Homo sapiens.  
XX  
PN WO200175110-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US10589.  
XX  
PR 30-MAR-2000; 2000US-0538913.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Hoogenboom HRJM, Henderikx MPG;  
XX  
DR WPI; 2001-626437/72.  
XX  
DR N-PSDB; AAD20745.  
XX  
PT Novel isolated tumor-associated antigen mucin-1-specific binding member  
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
PT its portion for binding to an epitope of the protein core of mucin-1 -

XX PS Claim 12: Page 106-108; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and x-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

XX CC binding member is useful for diagnosing and imaging MUC1-expressing

XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,

XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

XX CC containing molecules, and for therapeutically or prophylactically

XX CC treating cancer. The present sequence is human recombinant immunoglobulin

XX CC (Ig) heavy chain region (variable VH and CH constant heavy chain).

XX SQ Sequence 451 AA;

Query Match 100.0%; Score 451; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWYRQAPGKLEWVSGISGGSTYY 60

Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWYRQAPGKLEWVSGISGGSTYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYIQMNSLRAREDYAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRAREDYAVYYCAKHTGGGVWDPIDYWGQGLTVTS 120

Qy 121 SASTKGPSVFFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180

Db 121 SASTKGPSVFFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180

Qy 181 SGLYSLSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKHTCCPCPAPELLG 240

Db 181 SGLYSLSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKHTCCPCPAPELLG 240

Qy 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGEVHNKATKPREEQY 300

Db 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGEVHNKATKPREEQY 300

Qy 301 NSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360

Db 301 NSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360

Qy 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR 420

Db 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR 420

Qy 421 WQGGNVFSCSVNMEALHNHYTQKSLSLSPGK 451

Db 421 WQGGNVFSCSVNMEALHNHYTQKSLSLSPGK 451

RESULT 2

AAU007745

ID AAU007745 standard; Protein; 461 AA.

XX AC AAU007745;

XX AC AAU007745;

XX AC AAU007745;

DT 04-DEC-2001 (first entry)

XX Humanised monoclonal antibody Hu266, heavy chain.

DE Monoclonal antibody; Hu266; nontropic; neuroprotective; Abeta peptide;

XX Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;

KW gene therapy.

XX Mus sp.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= signal\_peptide

FT Protein 20..461

FT /label= Mature\_Hu266\_heavy\_chain

FT /note= "this sequence is specifically claimed in claim 17"

XX WO200162801-A2.

XX 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US06191.

XX 24-FEB-2000; 2000US-0184601.

PR 08-DEC-2000; 2000US-0254465.

PR 08-DEC-2000; 2000US-0254498.

XX (UNIW ) UNIV WASHINGTON.

PA (ELIL ) LILLY & CO ELI.

XX Holtzman DM, Demattos R, Baies KR, Paul SM, Tsurushita N;

PI Vasquez M;

PI WPI; 2001-550087/61.

XX New humanised antibody for the treatment of Alzheimer's comprises the inhibition and reduction of the formation of amyloid plaques -

XX Example 13; Fig 5; 63pp; English.

XX The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicament. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy.

CC Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.

XX SQ Sequence 461 AA;

Query Match 76.1%; Score 343; DB 22; Length 461;

Best Local Similarity 100.0%; Pred. No. 2.9e-246;

Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 DYWGQGLTVTVSSASTKGPSVFFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT 168

Db 119 DYWGQGLTVTVSSASTKGPSVFFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT 178

Qy 169 SGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKTH 228

Db 179 SGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKTH 238

Qy 229 TCPCPCAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGEV 288

Db 239 TCPCPCAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGEV 298

Qy 289 HNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPR 348

Db 299 HNAKTKPREEQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPR 358

Qy 349 EPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPVLDSDGSF 408

|||||  
Db 359 EFQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPNKYKTPPVLDSGSEF 418  
QY 409 FLYSKLTVDKSRWQOGNVFSCVMHEALHNYHTOKSLSPGK 451  
Db 419 FLYSKLTVDKSRWQOGNVFSCVMHEALHNYHTOKSLSPGK 461  
RESULT 3  
AA43339  
ID AAR43339 standard; Protein; 449 AA.  
XX  
AC AAR43339;  
XX  
DT 29-NOV-1993 (first entry)  
XX  
DE Completely humanised C4G1 Ig heavy chain.  
XX  
KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;  
KW monoclonal antibody; platelet agglutination; humanised antibody.  
XX  
OS Synthetic.  
XX  
PN WO9313133-A.  
XX  
PD 08-JUL-1993.  
XX  
PF 15-DEC-1992; 92WO-JP01630.  
XX  
PR 20-DEC-1991; 91US-0812111.  
PR 09-JUN-1992; 92US-0895952.  
PR 11-SEP-1992; 92US-0944159.  
XX  
(PROT-) PROTEIN DESIGN LABS INC.  
PA (YAMA) YAMANOUCHI PHARM CO LTD.  
XX  
PI Co MS, Tso JY;  
XX  
DR WPI; 1993-227275/28.  
XX  
XX Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa  
PT protein - for treating disorders related to vascular thrombosis  
PS Claim 26; Fig 5C; 54pp; Japanese.  
XX  
This is the sequence of the humanised C4G1 immunoglobulin heavy  
CC chain fragment. See AAR43338 for the light chain sequence. The  
CC antibody is specific for the platelet membrane glycoprotein  
CC GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus  
CC useful in the treatment of thrombosis.  
XX  
SQ Sequence 449 AA;  
Query Match 75.8%; Score 342; DB 14; Length 449;  
Best Local Similarity 100.0%; Pred. No. 1.5e-245;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YWQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTS 169  
Db 108 YWQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTS 167  
QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHT 229  
Db 168 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHT 227  
QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289  
Db 228 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 287  
QY 290 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEIKTSKAKGPRE 349  
Db 288 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPKEIKTSKAKGPRE 347

QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPNKYKTPPVLDSGSEF 409  
Db 348 PQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPNKYKTPPVLDSGSEF 407  
QY 410 LYSKLTVDKSRWQOGNVFSCVMHEALHNYHTOKSLSPGK 451  
Db 408 LYSKLTVDKSRWQOGNVFSCVMHEALHNYHTOKSLSPGK 449  
RESULT 4  
AAW49816  
ID AAW49816 standard; Protein; 449 AA.  
XX  
AC AAW49816;  
XX  
DT 24-SEP-1998 (first entry)  
XX  
DE Amino acid sequence of the humanised antibody C4G1 heavy chain.  
XX  
KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;  
KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;  
KW thromboembolic disorder; cancer; acute myocardial infarction;  
KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;  
KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX  
PN US5777085-A.  
XX  
PD 07-JUL-1998.  
XX  
PF 17-MAY-1995; 95US-0458516.  
XX  
PR 03-MAY-1993; 93US-0059159.  
PR 20-DEC-1991; 91US-0812111.  
PR 09-JUN-1992; 92US-0895952.  
PR 11-SEP-1992; 92US-0944159.  
XX  
(PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Co MS, Tso JY;  
XX  
DR WPI; 1998-398136/34.  
XX  
New humanised immunoglobulin which binds GPIIb/IIIa - derived from  
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for  
PT treating cardiovascular and thromboembolic disorders.  
XX  
PS Claim 4; Fig 5D; 35pp; English.  
XX  
This is the amino acid sequence of the humanised antibody C4G1 heavy  
CC chain, used in the method of the invention involving the creation  
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.  
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting  
CC platelet aggregation and also the releasing reaction of platelets. The  
CC Ig can be used for treating cardiovascular diseases and thromboembolic  
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,  
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,  
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in  
CC diagnosing the presence and location of a thrombus, or certain types of  
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the  
CC detection of GPIIb/IIIa antigens or for isolating platelets.  
XX  
SQ Sequence 449 AA;  
Query Match 75.8%; Score 342; DB 19; Length 449;  
Best Local Similarity 100.0%; Pred. No. 1.5e-245;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YWQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTS 169  
Db 108 YWQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTS 167

QY 170 GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVKVPKSCDKTHT 229  
 Db 168 GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVKVPKSCDKTHT 227  
 QY 230 CPPCPAPELLGGPSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289  
 Db 228 CPPCPAPELLGGPSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 287  
 QY 290 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 349  
 Db 288 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 347  
 QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 409  
 Db 348 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 407  
 QY 410 LYSKLTVDKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 451  
 Db 408 LYSKLTVDKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 449

RESULT 5  
 AAR93553 standard; Protein; 475 AA.  
 AC AAR93553;  
 XX 20-AUG-1996 (first entry)  
 DT Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.  
 DE Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;  
 KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Peptide 1..19 /note= "Signal peptide"  
 FT Protein 20..475  
 FT /note= "Mature heavy chain"

XX JP08038178-A.  
 XX 13-FEB-1996.  
 XX 20-FEB-1995; 95JP-0030742.  
 XX 18-FEB-1994; 94JP-0021628.  
 XX (NISN ) NISSHINBO IND INC.  
 XX (TANA/) TANAKA H.  
 XX WPI; 1996-154852/16.  
 XX N-PSDB; AAT18059.  
 XX Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
 PT produced by primer amplification, used in the diagnosis of hCMV  
 PT infection  
 XX Claim 4; Page 16-18; 22pp; Japanese.  
 XX The sequences given in AAR93553-54 represent the heavy and light chains  
 CC respectively of a monoclonal antibody against a 65 kD antigen of human  
 CC cytomegalovirus (hCMV). The DNA's encoding these sequences were  
 CC amplified using the sequences given in AAR18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hCMV.  
 XX Sequence 475 AA;

Query Match 75.8%; Score 342; DB 17; Length 475;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-245;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 110 YMQQGTFLVTSSASTKGPSPFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTS 169  
 Db 134 YMQQGTFLVTSSASTKGPSPFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTS 193  
 QY 170 GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVKVPKSCDKTHT 229  
 Db 194 GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVKVPKSCDKTHT 253  
 QY 230 CPPCPAPELLGGPSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289  
 Db 254 CPPCPAPELLGGPSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 313  
 QY 290 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 349  
 Db 314 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 373  
 QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 409  
 Db 374 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 433  
 QY 410 LYSKLTVDKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 451  
 Db 434 LYSKLTVDKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 475

RESULT 6  
 AAB81972 standard; Protein; 581 AA.  
 AC AAB81972;  
 DT 03-JUL-2001 (first entry)  
 DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.  
 XX Ganglioside; GD2; complementation determining region; CDR; antibody;  
 KW mouse; cancer.  
 XX Synthetic.  
 XX WO200123573-A1.  
 XX 05-APR-2001.  
 XX 29-SEP-2000; 2000WO-JP06773.  
 XX 30-SEP-1999; 99JP-0278290.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX WPI; 2001-266163/27.

XX Human type complementation-determining domain transplanted antibody and  
 PT derivatives against ganglioside GD2, useful in diagnosis and therapy of  
 PT e.g. tumours, has low antigenicity, little side effects but potent  
 PT activity in cancer -  
 XX Example 3; Page 111-114; 123pp; Japanese.  
 XX The present invention describes an antibody, which can react specifically  
 CC with ganglioside GD2, and is transplanted with a human type  
 CC complementation-determining domain (CDR), or its fragments. The antibody  
 CC and its derivatives are useful in diagnosis and therapy of tumours,  
 CC particularly cancer diagnosis. The present sequence is a protein  
 CC used in the exemplification of the invention.  
 XX Sequence 581 AA;

Query Match 75.8%; Score 342; DB 22; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-245;

Best Local Similarity 100.0%; Pred. No. 1.9e-245; Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 110 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTS 169	
Db 107 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTS 166	
Qy 170 GVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 229	
Db 167 GVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 226	
Qy 230 CPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289	
Db 227 CPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 286	
Qy 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349	
Db 287 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 346	
Qy 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 409	
Db 347 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 406	
Qy 410 LYSKLTVDKSRWQOGNWFSCSVMHREALHNYTKQSLSPGK 451	
Db 407 LYSKLTVDKSRWQOGNWFSCSVMHREALHNYTKQSLSPGK 448	
RESULT 7	
AAB83156	
ID AAB83156 standard; protein.: 583 AA.	
XX AAB83156;	
XX 02-JUL-2001 (first entry)	
DT ganglioside GM2 antibody-related protein #1.	
DE Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.	
XX Unidentified.	
OS WO200123431-A1.	
XX 05-APR-2001.	
XX 29-SEP-2000; 2000WO-JP06775.	
XX 30-SEP-1999; 99JP-0278292.	
XX (KYOW ) KYOWA HAKKO KOGYO KK.	
XX Hanai N, Nakamura K, Niwa R;	
XX WPI; 2001-266142/27.	
XX Monoclonal antibodies against ganglioside GM2 combined with drugs,	
PT radioisotopes or proteins for treatment and diagnosis of cancer -	
XX Claim 43; Page 61-65; 80pp; Japanese.	
XX The present invention relates to derivatives of an antibody against	
CC ganglioside GM2. The antibody may be a monoclonal antibody or its	
CC fragments. The antibody is combined with a radioactive isotope,	
CC protein or small drug in the treatment and diagnosis of cancer.	
XX Sequence 583 AA;	
Query Match 75.8%; Score 342; DB 22; Length 583;	
Best Local Similarity 100.0%; Pred. No. 1.9e-245; Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 110 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTS 169	

Best Local Similarity 100.0%; Pred. No. 1.9e-245; Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db 109 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTS 168	
Qy 170 GVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 229	
Db 169 GVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 228	
Qy 230 CPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289	
Db 229 CPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 288	
Qy 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349	
Db 289 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 348	
Qy 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 409	
Db 349 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 408	
Qy 410 LYSKLTVDKSRWQOGNWFSCSVMHREALHNYTKQSLSPGK 451	
Db 409 LYSKLTVDKSRWQOGNWFSCSVMHREALHNYTKQSLSPGK 450	
RESULT 8	
AAM52156	
ID AAM52156 standard; Protein; 731 AA.	
XX AAM52156;	
XX 05-FEB-2002 (first entry)	
DT Humanised HMFG-1 heavy chain/DNase I fusion protein 1.	
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;	
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.	
XX Homo sapiens.	
OS Synthetic.	
XX WO200174905-A1.	
XX 11-OCT-2001.	
XX 26-MAR-2001; 2001WO-GB01324.	
XX 03-APR-2000; 2000GB-0008049.	
PR 02-OCT-2000; 2000US-237159P.	
XX (ANTI-) ANTISOMA RES LTD.	
XX Young RJ;	
PI WPI; 2001-662969/76.	
DR Novel compound used to treat cancer has target cell-specific portion	
PT comprising humanised monoclonal antibody having specificity for	
PT polymorphic epithelial mucin, and cytotoxic portion having	
PT endonucleolytic activity -	
XX Claim 20; Figure 7; 176pp; English.	
XX The invention relates to a compound which comprises a target	
CC cell-specific portion, comprising an humanised monoclonal antibody,	
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen	
CC binding fragment and a cytotoxic portion having endonucleolytic activity,	
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The	
CC compound has cytostatic activity useful for treating cancer and acting as	
CC a potential inducer of apoptosis.	
XX Sequence 731 AA;	
Query Match 75.8%; Score 342; DB 22; Length 731;	

[illegible]



CC with expression of CD81, or CD81. This substance is especially an  
 CC antibody with affinity towards HCV E2/NS1 protein, containing amino  
 CC acid sequences based on the complementarity determining region (CDR) 1,  
 CC CDR2 and CDR3 of the H and L chain variable regions. The antibody  
 CC inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.  
 CC The antibodies and drugs are used for treatment and/or prevention of  
 CC hepatitis C, or for diagnosis of hepatitis C.

XX SQ Sequence 475 AA;

Query Match 75.6%; Score 341; DB 22; Length 475;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WQGGTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSG 170  
 Db 135 WQGGTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSG 194

QY 171 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVPEKSCDKTHTC 230  
 Db 195 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVPEKSCDKTHTC 254

QY 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
 Db 255 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 314

QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
 Db 315 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 374

QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 410  
 Db 375 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 434

QY 411 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
 Db 435 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 11  
 ID AAR31023  
 AC AAR31023;  
 XX  
 XX 19-MAY-1993 (first entry)  
 XX Antibody D heavy chain.

KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;  
 KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;  
 KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.

OS Synthetic.

Key	Location/Qualifiers
FT Peptide	1..19
FT Region	/note= "Signal peptide"
FT	20..49
FT	/label= FR1
FT	50..54
FT	/label= CDR1
FT	55..68
FT	/label= FR2
FT	69..84
FT	/label= CDR2
FT	85..113
FT	/label= FR3
FT	114..121
FT	/label= CDR3
FT	122..132
FT	/label= FR4
FT	133..241
FT	Domain

FT Region /label= CH1  
 FT 242..262  
 FT /label= HINGE  
 FT Domain 263..379  
 FT /label= CH2  
 FT Domain 380..497  
 FT /label= CH3  
 XX  
 PN EP523949-A.  
 XX  
 XX 20-JAN-1993.  
 XX  
 PF 14-JUL-1992; 92EP-0306420.  
 XX  
 PR 15-JUL-1991; 91GB-0015284.  
 PR 01-AUG-1991; 91GB-0016594.  
 PR 23-MAR-1992; 92GB-0006284.  
 XX  
 PA (WELL ) WELLCOME FOUND LTD.  
 XX  
 PI Crowe JS, Lewis AP;  
 XX  
 DR WPI; 1993-019951/03.  
 DR N-PSDB; AAQ35099.  
 XX  
 PT Prodn. of recombinant primate antibodies - useful for treating  
 PT infections caused by hepatitis A, B and C, herpes,  
 PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,  
 PT arthritis etc.  
 XX  
 PS Disclosure; Fig 2; 35pp; English.  
 XX  
 CC The sequences given in AAR31023-24 represent the heavy and light chains  
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which  
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus  
 CC (HAV) sero positive patient. Antibody D is closely related in nature  
 CC to murine antibody B5B3. Total RNA was isolated from antibody D  
 CC expressing cells and polyadenylated RNA was extracted. These polyA  
 CC RNA's were used to prepare a cDNA library which was screened for human  
 CC kappa light (L) chains and two positive clones were detected.  
 CC Further heavy (H) chain clones were also isolated.  
 XX  
 SQ Sequence 476 AA;

Query Match 75.6%; Score 341; DB 14; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WQGGTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSG 170  
 Db 136 WQGGTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSG 195

QY 171 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVPEKSCDKTHTC 230  
 Db 196 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVPEKSCDKTHTC 255

QY 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
 Db 256 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 315

QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
 Db 316 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 375

QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 410  
 Db 376 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 435

QY 411 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
 Db 436 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 476

Query Match	75.6%;	Score 341;	DB 13;	Length 481;
Best Local Similarity	100.0%;	Pred. No. 8.9e-245;		

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SQ Sequence 729 AA;
Query Match 75.6%; Score 341; DB 22; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.2e-244;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMQGTLTVTSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTS 169
    |||||
DB 126 YMQGTLTVTSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTS 185
    |||||
QY 170 GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 229
    |||||
DB 186 GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 245
    |||||
QY 230 CPPCPAPELGGPSVFLPPPKDLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVH 289
    |||||
DB 246 CPPCPAPELGGPSVFLPPPKDLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVH 305
    |||||
QY 290 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
    |||||
DB 306 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365
    |||||
QY 350 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 409
    |||||
DB 366 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 425
    |||||
QY 410 LYSKLTVDKSRWQOGNVPFSCSVMHREALHNYTQKSLSLSPG 450
    |||||
DB 426 LYSKLTVDKSRWQOGNVPFSCSVMHREALHNYTQKSLSLSPG 466
    |||||

RESULT 14
AAM52161
ID AAM52161 standard; Protein; 739 AA.
XX
AC AAM52161;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 6.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200174905-A1.
XX
XX 11-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
XX
XX 02-OCT-2000; 2000US-237159P.
XX
XX {ANTI-} ANTISOMA RES LTD.
XX
XX Young RJ;
XX
XX WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity
XX
XX Claim 20; Figure 12; 176pp; English.
XX
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity.
XX

CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 739 AA;
Query Match 75.6%; Score 341; DB 22; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.2e-244;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMQGTLTVTSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTS 169
    |||||
DB 126 YMQGTLTVTSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTS 185
    |||||
QY 170 GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 229
    |||||
DB 186 GVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 245
    |||||
QY 230 CPPCPAPELGGPSVFLPPPKDLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVH 289
    |||||
DB 246 CPPCPAPELGGPSVFLPPPKDLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVH 305
    |||||
QY 290 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
    |||||
DB 306 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365
    |||||
QY 350 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 409
    |||||
DB 366 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 425
    |||||
QY 410 LYSKLTVDKSRWQOGNVPFSCSVMHREALHNYTQKSLSLSPG 450
    |||||
DB 426 LYSKLTVDKSRWQOGNVPFSCSVMHREALHNYTQKSLSLSPG 466
    |||||

RESULT 15
AAM52157
ID AAM52157 standard; Protein; 730 AA.
XX
AC AAM52157;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 2.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200174905-A1.
XX
XX 11-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
XX
XX 02-OCT-2000; 2000US-237159P.
XX
XX {ANTI-} ANTISOMA RES LTD.
XX
XX Young RJ;
XX
XX WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity
XX
XX Claim 20; Figure 8; 176pp; English.
XX
```

CC The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.

XX	Sequence	730 AA;
SQ	Query Match	75.4%; Score 340; DB 22; Length 730;
	Best Local Similarity	100.0%; Pred. No. 6.8e-244;
	Matches 340; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	110	YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS 169
Db	126	YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS 185
Qy	170	GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 229
Db	186	GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 245
Qy	230	CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 289
Db	246	CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 305
Qy	290	NAKTKPREEQYNSTYRVVSVLTVQLHQLWLNQKEYCKVSNKALPAPTEKTIISKAKGQPRE 349
Db	306	NAKTKPREEQYNSTYRVVSVLTVQLHQLWLNQKEYCKVSNKALPAPTEKTIISKAKGQPRE 365
Qy	350	PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 409
Db	366	PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 425
Qy	410	LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 449
Db	426	LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 465

Search completed: October 9, 2002, 19:23:02  
Job time : 50.3214 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 18.4082 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALNHYTKQSLSPGK 451

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 2442594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343	76.1	446	3	US-08-397-411-7
2	342	75.8	449	1	US-08-458-516-13
3	341	75.6	476	2	US-08-378-939-10
4	338	74.9	371	1	US-08-236-311-7
5	338	74.9	371	3	US-08-457-918-7
6	283	62.7	459	1	US-08-157-101A-7
7	251	55.7	449	4	US-08-679-397-2
8	249	55.2	451	2	US-08-887-352B-14
9	249	55.2	451	2	US-08-887-352B-16
10	249	55.2	451	2	US-08-887-352B-18
11	249	55.2	451	3	US-08-466-151-65
12	249	55.2	451	4	US-09-109-207C-14
13	249	55.2	451	4	US-09-109-207C-16
14	249	55.2	451	4	US-09-109-207C-18
15	249	55.2	451	4	US-09-282-505-2
16	249	55.2	451	4	US-09-054-255-2
17	249	55.2	451	4	US-09-296-005-14
18	249	55.2	451	4	US-09-296-005-16
19	249	55.2	451	4	US-09-296-005-18
20	249	55.2	452	3	US-09-027-449-71
21	249	55.2	452	4	US-09-026-985-71
22	243	53.9	454	2	US-07-934-373C-22
23	243	53.9	454	3	US-08-437-642B-22
24	243	53.9	454	5	PCT-US93-07832-22
25	243	53.9	467	4	US-09-049-672A-8
26	236	52.3	442	5	PCT-US96-10043-9
27	235	52.1	453	3	US-08-466-151-8

ALIGNMENTS

RESULT 1  
US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispesific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 76.1%; Score 343; DB 3; Length 446;  
Best Local Similarity 100.0%; Pred. No. 4.6e-238;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 8, Appli  
Sequence 4, Appli  
Sequence 12, Appli  
Sequence 8, Appli  
Sequence 50, Appli  
Sequence 2, Appli  
Sequence 11, Appli  
Sequence 22, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 12, Appli  
Sequence 14, Appli  
Sequence 11, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 6, Appli  
Sequence 43, Appli  
Sequence 43, Appli

QY 109 DYWGQGLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALT 168  
DB 104 DYWGQGLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALT 163  
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTH 228  
DB 164 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTH 223  
QY 229 TCPPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 288  
DB 224 TCPPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 283  
QY 289 HNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348  
DB 284 HNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 343  
QY 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
DB 344 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 403  
QY 409 FLYSKLTVDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 451  
DB 404 FLYSKLTVDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 446

## RESULT 2

US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co. Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIb/IIIa  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRES:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-13

-Query Match 75.8%; Score 342; DB 1; Length 449;  
Best Local Similarity 100.0%; Pred. No. 2.4e-237;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YWGQGLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALT 169  
DB 108 YWGQGLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALT 167  
QY 170 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTH 229  
DB 168 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTH 227  
QY 230 CPPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 289  
DB 228 CPPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 287  
QY 290 NAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 349  
DB 288 NAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 347  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 409  
DB 348 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 407  
QY 410 LYSKLTVDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 451  
DB 408 LYSKLTVDKSRWQOGNPFSCSVNHEALHNHYTQKSLSLSPGK 449

RESULT 3  
US-08-378-939-10  
; Sequence 10, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROME, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-378-939-10

Query Match 75.6%; Score 341; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.3e-236;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 111 WGGTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170
Db 136 WGGTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 195
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTC 230
Db 196 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTC 255
QY 231 PCPAPPELLGGPSVFLFPPPKDPTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Db 256 PCPAPPELLGGPSVFLFPPPKDPTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 315
QY 291 AKTKPREQYNSTRYVVSIVTLVHQLDMLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREP 350
Db 316 AKTKPREQYNSTRYVVSIVTLVHQLDMLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREP 375
QY 351 QYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL 410
Db 376 QYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL 435
QY 411 YSKLTVDKSRWQOGNVFSCSVMHREALHNYHTQKSLSLSPGK 451
Db 436 YSKLTVDKSRWQOGNVFSCSVMHREALHNYHTQKSLSLSPGK 476

RESULT 4
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5365335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-7

Query Match 74.98; Score 338; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.5e-234;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 173
Db 34 GTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 93
QY 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPC 233
Db 94 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPC 153
QY 234 PAPELLGGPSVFLFPPPKDPTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT 293
Db 154 PAPELLGGPSVFLFPPPKDPTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT 213
QY 294 KPREEQYNSTRYVVSIVTLVHQLDMLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVY 353
Db 214 KPREEQYNSTRYVVSIVTLVHQLDMLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVY 273
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
Db 274 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 333
QY 414 LTVDKSRWQOGNVFSCSVMHREALHNYHTQKSLSLSPGK 451
Db 334 LTVDKSRWQOGNVFSCSVMHREALHNYHTQKSLSLSPGK 371

RESULT 5
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
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; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

Query Match 74.9%; Score 338; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.5e-234;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 173
Db 34 GTLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 93
QY 174 FPAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTPCC 233
Db 94 FPAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTPCC 153
QY 234 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
Db 154 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 213
QY 294 KPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVY 353
Db 214 KPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVY 273
QY 354 TLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413
Db 274 TLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 333
QY 414 LTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 334 LTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371

RESULT 6
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NORIO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994

; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 62.7%; Score 283; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 3.6e-195;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 SGVHTEPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTH 228
Db 177 SGVHTEPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTH 236
QY 229 TCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288
Db 237 TCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 296
QY 289 HNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPR 348
Db 297 HNAKTKPREEQYNSTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIETKISKAKGQPR 356
QY 349 EPOYVITLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 408
Db 357 EPOYVITLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 416
QY 409 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 417 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 459

RESULT 7
US-09-679-397-2
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: PL241R1D2
; CURRENT APPLICATION NUMBER: US/09/679,397
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match 55.7%; Score 251; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.7e-172;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 DYWGOGTLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT 168
Db 109 DYWGOGTLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT 168
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Db 108 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALT 167  
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTH 228  
Db 168 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTH 227  
QY 229 TCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 288  
Db 228 TCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 287  
QY 289 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348  
Db 288 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 347  
QY 349 EPQVTLPPSR 359  
Db 348 EPQVTLPPSR 358  
RESULT 8  
US-08-887-352B-14  
; Sequence 14, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe  
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-14  
Query Match 55.2%; Score 249; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSG 170  
Db 111 WQGTGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
QY 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359  
RESULT 9  
US-08-887-352B-16  
; Sequence 16, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe  
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-16  
Query Match 55.2%; Score 249; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSG 170  
Db 111 WQGTGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
QY 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

RESULT 10  
US-08-887-352B-18  
; Sequence 18, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-18  
Query Match 55.2%; Score 249; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTPLTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
Db 111 WQGTPLTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHC 230  
Db 171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHC 230  
QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359  
RESULT 11  
US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardiou, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P07182C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-65  
Query Match 55.2%; Score 249; DB 3; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTPLTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
Db 111 WQGTPLTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHC 230  
Db 171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHC 230  
QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359  
RESULT 12  
US-09-109-207C-14  
; Sequence 14, Application US/09109207C

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: Patent No. 6172213
:
: GENERAL INFORMATION:
:
: APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
:
: TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptide
:
: FILE REFERENCE: P1123R1
:
: CURRENT APPLICATION NUMBER: US/09/109, 207C
:
: CURRENT FILING DATE: 1998-06-30
:
: PRIOR APPLICATION NUMBER: US 60/051,554
:
: PRIOR FILING DATE: 1997-07-03
:
: NUMBER OF SEQ ID NOS: 44
:
: SEQ ID NO 14
:
: LENGTH: 451
:
: TYPE: PRT
:
: ORGANISM: Artificial
:
: FEATURE:
:
: NAME/KEY: Artificial
:
: LOCATION: 1-451
:
: OTHER INFORMATION: Heavy chain sequence derived from MAE11
:
: US-09-109-207C-14

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Query Match	55.2%	Score 249;	DB 4;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 7.2e-171;		
Matches 249;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	111	WGOGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSG	170	
Db	111	WGOGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSG	170	
QY	171	VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC	230	
Db	171	VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC	230	
QY	231	PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVQVDSVEDPEVKENWYVDGVEVHN	290	
Db	231	PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVQVDSVEDPEVKENWYVDGVEVHN	290	
QY	291	AKTKPREEQINSTYRVWSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTIISAKAGQPREP	350	
Db	291	AKTKPREEQINSTYRVWSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTIISAKAGQPREP	350	
QY	351	QVYTLPPPSR	359	
Db	351	QVYTLPPPSR	359	

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RESULT 13
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123r1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

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Query Match      55.28;  Score 249;  DB 4;  Length 451;
Best Local Similarity 100.0%;  Pred. No. 7.2e-171;
Matches 249;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  111  WGGGLTVTVSSASTKGPSVFPLAPSSKSTGGTAAAGCLVKDYFPPETVTVNSGALTSG 170

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Db	111	WGQGTLTWTVSSASTKGPSYFPLAPSSKSTSGTGAALGCLVKDYFPEPVTWVSNNSGALTSG	170
Qy	171	VHTFPVAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHNKPSNTKVDKKEPKSCDKHTTC	230
Db	171	VHTFPVAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHNKPSNTKVDKKEPKSCDKHTTC	230
Qy	231	PPCPAPELGGPSVFLFPPPKADTLIMISRTPEVTCVVVDVSHEDPSVKENWYVDGVEVHN	290
Db	231	PPCPAPELGGPSVFLFPPPKADTLIMISRTPEVTCVVVDVSHEDPSVKENWYVDGVEVHN	290
Qy	291	AKTKPREEQNSTYRNVSVLTVLVDHWLNGKEYCKVSKNSKALPAPIEKTISKAKGQPREP	350
Db	291	AKTKPREEQNSTYRNVSVLTVLVDHWLNGKEYCKVSKNSKALPAPIEKTISKAKGQPREP	350
Qy	351	QVYTLPPSR	359
Db	351	QVYTLPPSR	359

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RESULT 14
US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123P1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-18

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Query Match	55.2%	Score 249;	DB 4;	Length 451;
Best Local Similarity	100.0%;	Pred. No. 7.2e-171;		
Matches 249;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	111	WGOGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNNSGALTSG	170	
Db	111	WGOGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNNSGALTSG	170	
Qy	171	VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHFTC	230	
Db	171	VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHFTC	230	
Qy	231	PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHN	290	
Db	231	PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHN	290	
Qy	291	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKSNKALPAPTEKTIISKAKGQPREP	350	
Db	291	AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKSNKALPAPTEKTIISKAKGQPREP	350	
Qy	351	QVYTLPPSR	359	
Db	351	QVYTLPPSR	359	

RESULT 15  
US-09-282-505-2  
; Sequence 2, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:

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; APPLICANT: Esho Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Query Match      55.2%; Score 249; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 7.2e-171; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WQGGTLVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170
Db 111 WQGGTLVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170

Qy 171 VHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTC 230
Db 171 VHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTC 230

Qy 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Db 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy 291 AKTKPREEQYNSTYRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Db 291 AKTKPREEQYNSTYRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy 351 QVYTLPPSR 359
Db 351 QVYTLPPSR 359
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Job time : 19.4082 secs

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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:10 ; Search time 177,179 Seconds  
(without alignments)  
895.951 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVOLVQSGGLVQPGGSLRL.....MHEALHNHYTKSLSPCK 451

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*  
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11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*  
24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	451	100.0	451	22	US-09-822-698A-26
2	343	76.1	446	20	US-09-618-380-7
3	343	76.1	494	21	US-09-760-479-636
4	342	75.8	449	3	US-07-944-159-23
5	342	75.8	731	22	US-09-825-012-46
6	342	75.8	741	22	US-09-825-012-55
7	341	75.6	481	21	US-09-760-479-644

8	341	75.6	729	22	US-09-825-012-52	Sequence 52, Appl
9	341	75.6	739	22	US-09-825-012-61	Sequence 61, Appl
10	340	75.4	730	22	US-09-825-012-49	Sequence 49, Appl
11	340	75.4	740	22	US-09-825-012-58	Sequence 58, Appl
12	338	74.9	371	3	US-07-885-959-7	Sequence 7, Appl
13	338	74.9	371	16	US-09-275-310-7	Sequence 7, Appl
14	338	74.9	430	21	US-09-760-479-715	Sequence 715, App
15	336	74.5	467	4	US-08-030-175-41	Sequence 41, Appl
16	336	74.5	467	4	US-08-030-175-42	Sequence 42, Appl
17	336	74.5	480	21	US-09-760-479-637	Sequence 637, App
18	335	74.3	447	21	US-09-760-479-623	Sequence 623, App
19	335	74.3	475	7	US-08-309-530-4	Sequence 4, Appl
20	335	74.3	476	15	US-09-111-286-3	Sequence 3, Appl
21	335	74.3	476	26	US-60-051-945-3	Sequence 3, Appl
22	335	74.3	499	21	US-09-760-479-645	Sequence 645, App
23	334	74.1	663	1	PCT-US01-32140-32	Sequence 32, Appl
24	334	74.1	4852	1	PCT-US01-32140-33	Sequence 33, Appl
25	333	73.8	474	21	US-09-760-479-655	Sequence 655, App
26	330	73.2	330	19	US-09-569-343-29	Sequence 29, Appl
27	330	73.2	330	19	US-09-569-343A-29	Sequence 29, Appl
28	330	73.2	330	22	US-09-892-949-38	Sequence 38, Appl
29	330	73.2	379	4	US-08-057-292-3	Sequence 3, Appl
30	330	73.2	447	16	US-09-256-156-1	Sequence 1, Appl
31	330	73.2	473	21	US-09-760-479-578	Sequence 578, App
32	330	73.2	541	1	PCT-US02-07214-32	Sequence 32, Appl
33	330	73.2	547	21	US-09-746-359A-54	Sequence 54, Appl
34	330	73.2	547	23	US-09-951-268-40	Sequence 40, Appl
35	330	73.2	558	1	PCT-US02-07214-31	Sequence 31, Appl
36	330	73.2	567	19	US-09-543-320-16	Sequence 16, Appl
37	330	73.2	567	22	US-09-825-561A-16	Sequence 16, Appl
38	330	73.2	571	21	US-09-746-359A-53	Sequence 53, Appl
39	330	73.2	571	23	US-09-951-268-30	Sequence 30, Appl
40	330	73.2	951	9	US-08-563-105-8	Sequence 8, Appl
41	330	73.2	951	15	US-09-177-009-8	Sequence 8, Appl
42	330	73.2	951	17	US-09-313-942-9	Sequence 9, Appl
43	326	72.3	470	16	US-09-238-741-4	Sequence 4, Appl
44	319	70.7	470	15	US-09-107-223A-2	Sequence 2, Appl
45	283	62.7	459	5	US-08-157-101-7	Sequence 7, Appl

#### ALIGNMENTS

RESULT 1  
US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1  
US-09-822-698A-26

Query Match 100.0%; Score 451; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLVWSIGSGSGSTYY 60  
Db 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPKGLVWSIGSGSGSTYY 60

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QY 61 ADSVKGRFTTISRNSKNTLYQWNSLRAEDTAVYYCAKHTGGGVWDPIDWGGQGLTVTVS 120
Db 61 ADSVKGRFTTISRNSKNTLYQWNSLRAEDTAVYYCAKHTGGGVWDPIDWGGQGLTVTVS 120
QY 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180
Db 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180
QY 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHHTCCPPCPAPPELLG 240
Db 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHHTCCPPCPAPPELLG 240
QY 241 GPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 300
Db 241 GPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPREEQY 300
QY 301 NSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
Db 301 NSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
QY 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420
Db 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420
QY 421 WOQGNVFSCSVHMEALHNHYTQKSLSLSPGK 451
Db 421 WOQGNVFSCSVHMEALHNHYTQKSLSLSPGK 451
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RESULT 2
US-09-618-380-7
; Sequence 7, Application us/09618380
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
;             Gingrich, Roger
;             Link, Brian
;             Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
;                   B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,380
; FILING DATE: 18-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/397,411
; FILING DATE: 1995-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-618-380-7
Query Match          76.1%; Score 343; DB 20; Length 446:
Best Local Similarity 100.0%; Pred. No. 9.7e-311;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALT 168
Db 104 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALT 163
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTH 228
Db 164 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTH 223
QY 229 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 288
Db 224 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 283
QY 289 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348
Db 284 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 343
QY 349 EPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408
Db 344 EPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 403
QY 409 FLYSKLTVDKSRWQQGNVSCSVHMEALHNHYTQKSLSLSPGK 451
Db 404 FLYSKLTVDKSRWQQGNVSCSVHMEALHNHYTQKSLSLSPGK 446
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```
RESULT 3
US-09-760-479-636
; Sequence 636, Application us/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 636
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-636
Query Match          76.1%; Score 343; DB 21; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.1e-310;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALT 168
Db 152 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALT 211
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTH 228
Db 212 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTH 271
QY 229 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 288
Db 272 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 331
QY 289 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348
Db 332 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 391
QY 349 EPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408
Db 392 EPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 451
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QY 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
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Db 452 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 494  
|||||  
RESULT 4  
US-07-944-159-23  
; Sequence 23, Application US/07944159  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Iso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIb/IIIa  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/944,159  
; FILING DATE: 19920911  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30, 223  
; REFERENCE/DOCKET NUMBER: 11823-37-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-944-159-23

Query Match 75.8%; Score 342; DB 3; Length 449;  
Best Local Similarity 100.0%; Pred. No. 8.4e-310; Mismatches 0; Indels 0; Gaps 0;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 169  
|||||  
Db 108 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 167  
|||||  
QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHT 229  
|||||  
Db 168 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHT 227  
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QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 289  
Db 228 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 287  
|||||  
QY 290 NAKTKPREQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPRE 349  
Db 288 NAKTKPREQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPRE 347  
|||||  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
Db 348 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 407  
|||||  
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
|||||

Db 408 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 449  
|||||  
RESULT 5  
US-09-825-012-46  
; Sequence 46, Application US/09825012  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 46  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion  
US-09-825-012-46

Query Match 75.8%; Score 342; DB 22; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.3e-309; Mismatches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 169  
|||||  
Db 126 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 185  
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QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHT 229  
Db 186 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHT 245  
|||||  
QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 289  
Db 246 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 305  
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QY 290 NAKTKPREQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPRE 349  
Db 306 NAKTKPREQYNSTRYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPRE 365  
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QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
Db 366 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 425  
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QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
|||||  
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 467  
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RESULT 6  
US-09-825-012-55  
; Sequence 55, Application US/09825012  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 55  
; LENGTH: 741  
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-55

Query Match      75.8%; Score 342; DB 22; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 YWGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTS 169
Db 126 YWGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTS 185
Qy 170 GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHT 229
Db 186 GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHT 245
Qy 230 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 289
Db 246 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 305
Qy 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
Db 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365
Qy 350 PQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 409
Db 366 PQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 425
Qy 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 451
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 467

RESULT 7
US-09-760-479-644
; Sequence 644, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 644
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-644

Query Match      75.6%; Score 341; DB 21; Length 481;
Best Local Similarity 100.0%; Pred. No. 7.6e-309;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTS 170
Db 141 WGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTS 200
Qy 171 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTC 230
Db 201 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTC 260
Qy 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 290
Db 261 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 320
Qy 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 350
Db 321 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 380
Qy 351 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL 410
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Db 381 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFL 440
Qy 411 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 451
Db 441 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPGK 481

RESULT 8
US-09-825-012-52
; Sequence 52, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

Query Match      75.6%; Score 341; DB 22; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.1e-308;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 YWGQGLTVTVSSASTKGPVFLPAPSSKSTSGTAALGCLVKDYFPEPTVYSWNSGALTS 169
Db 126 YWGQGLTVTVSSASTKGPVFLPAPSSKSTSGTAALGCLVKDYFPEPTVYSWNSGALTS 185
Qy 170 GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHT 229
Db 186 GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHT 245
Qy 230 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 289
Db 246 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 305
Qy 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
Db 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365
Qy 350 PQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 409
Db 366 PQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFF 425
Qy 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPG 450
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKSLSPG 466

RESULT 9
US-09-825-012-61
; Sequence 61, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-61

Query Match          75.6%; Score 341; DB 22; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.1e-308;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 409
DB 366 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 450
DB 426 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 466

RESULT 10
US-09-825-012-49
; Sequence 49, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-236808
; CURRENT APPLICATION NUMBER: US/09/825,012
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-49

Query Match          75.4%; Score 340; DB 22; Length 730;
Best Local Similarity 100.0%; Pred. No. 9.4e-308;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 409
DB 366 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 449
DB 426 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 465

RESULT 12
US-07-885-959-7
; Sequence 7, Application US/07885959
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QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 409
DB 366 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 449
DB 426 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 465

RESULT 11
US-09-825-012-58
; Sequence 58, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-236808
; CURRENT APPLICATION NUMBER: US/09/825,012
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-58

Query Match          75.4%; Score 340; DB 22; Length 740;
Best Local Similarity 100.0%; Pred. No. 9.5e-308;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YGQGTLYTVSSASTKGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 409
DB 366 POWYTLPPSRDELTKNOVSLTCLVKGYFSDIAVWESNGQPENNYKTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 449
DB 426 LYSKLTVDKSRWQQGNFVSCSVMHREALHNYHTOKSLSLSP 465

RESULT 12
US-07-885-959-7
; Sequence 7, Application US/07885959
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QY 234 PAPELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
 Db 154 PAPELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 213  
 QY 294 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVY 353  
 Db 214 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVY 273  
 QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413  
 Db 274 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 333  
 QY 414 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
 Db 334 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 371

RESULT 14  
 US-09-760-479-715  
 ; Sequence 715, Application US/09760479  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT253  
 ; CURRENT APPLICATION NUMBER: US/09/760,479  
 ; CURRENT FILING DATE: 2001-01-16  
 ; Prior application data removed - refer to PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 946  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 715  
 ; LENGTH: 430  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-760-479-715

Query Match 74.9%; Score 338; DB 21; Length 430;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-306;  
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 114 GTLVTVSSASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173  
 Db 93 GTLVTVSSASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 152  
 QY 174 FPAVLQSSGLYSLSSVTVVPSSTLTGTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPPC 233  
 Db 153 FPAVLQSSGLYSLSSVTVVPSSTLTGTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPPC 212  
 QY 234 PAPELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
 Db 213 PAPELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 272  
 QY 294 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVY 353  
 Db 273 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVY 332  
 QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413  
 Db 333 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 392  
 QY 414 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
 Db 393 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 430

RESULT 15  
 US-08-030-175-41  
 ; Sequence 41, Application US/08030175  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gorman, Scott D.  
 ; APPLICANT: Clark, Michael R.  
 ; APPLICANT: Cobbold, Stephen P.  
 ; APPLICANT: Waldmann, Herman  
 ; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION

; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
 ; STREET: 555 13TH ST., NW Suite 701 East  
 ; CITY: Washington  
 ; STATE: D. C.  
 ; COUNTRY: U.S.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
 ; COMPUTER: IBM AT compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
 ; SOFTWARE: WordPerfect 5.0 (Dos Text)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/030,175  
 ; FILING DATE: 17-MAY-1993  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB91/01578  
 ; FILING DATE: 13-SEP-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ernst, Barbara G.  
 ; REGISTRATION NUMBER: 30,377  
 ; REFERENCE/DOCKET NUMBER: 1768-113  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)783-6040  
 ; TELEFAX: (202)783-6031  
 ; INFORMATION FOR SEQ ID NO: 41:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 467 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-030-175-41

Query Match 74.5%; Score 336; DB 4; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-304;  
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 LVTVSSASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 175  
 Db 132 LVTVSSASTKGPSVFPLDPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 191  
 QY 176 AVLOSGLYSLSSVTVVPSSTLTGTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPPCPA 235  
 Db 192 AVLOSGLYSLSSVTVVPSSTLTGTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPPCPA 251  
 QY 236 PELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 295  
 Db 252 PELLGGPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 311  
 QY 296 REEQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVYTL 355  
 Db 312 REEQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPTEKTIKAKGQPREPQVYTL 371  
 QY 356 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 415  
 Db 372 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 431  
 QY 416 VDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
 Db 432 VDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 467

Search completed: October 9, 2002, 19:32:01  
 Job time : 179.179 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:45 ; Search time 59.8265 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVOPGGSLRL.....MHEALHNHYTKLSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1006125 seqs, 276659714 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	343	76.1	442	1	PCT-US02-21323-12
2	343	76.1	442	1	PCT-US02-21323-21
3	343	76.1	442	1	PCT-US02-21324-12
4	343	76.1	442	1	PCT-US02-21324-21
5	343	76.1	442	1	PCT-US02-26321-12
6	343	76.1	442	1	PCT-US02-26321-16
7	343	76.1	449	1	PCT-US02-11853-12
8	343	76.1	453	1	PCT-US02-11854A-12
9	343	76.1	468	1	PCT-US02-11853-20
10	343	76.1	472	1	PCT-US02-11854A-20
11	343	76.1	494	6	US-10-206-008-636
12	342	75.6	450	1	PCT-US02-21281-18
13	341	75.6	448	1	PCT-US01-27352-2
14	341	75.6	473	5	US-09-791-537-118977
15	341	75.6	476	5	US-09-791-537-104528
16	341	75.6	481	6	US-10-206-008-644
17	338	74.9	371	6	US-10-097-044A-7
18	338	74.9	430	6	US-10-206-008-715
19	338	74.9	430	6	US-10-211-364-1052
20	336	74.5	465	6	US-10-031-355-5
21	336	74.5	465	6	US-10-031-355-12
22	336	74.5	470	5	US-09-791-537-108421
23	336	74.5	480	6	US-10-206-008-637
24	335	74.3	447	6	US-10-206-008-623
25	335	74.3	476	5	US-09-747-669-3
26	335	74.3	499	6	US-10-206-008-645

ALIGNMENTS

RESULT 1

PCT-US02-21323-12  
; Sequence 12, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: humanized 266 antibody preferred heavy chain  
PCT-US02-21323-12  
Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLVTVSSAKGPSVFPLAPSSKSTSGGTAALGLVCKDYFPEPVTVMNSGALT 168  
Db 100 DYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVCKDYFPEPVTVMNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTH 219  
Qy 229 TCPCPAPPELLGGPSVFLPPLPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYDGV 288  
Db 220 TCPCPAPPELLGGPSVFLPPLPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYDGV 279  
Qy 289 HNAKTKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTSIRAKGQPR 348  
Db 280 HNAKTKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTSIRAKGQPR 339  
Qy 349 EPQYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSF 408  
|||||

Db 340 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 442

RESULT 2  
PCT-US02-21323-21  
; Sequence 21, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: heavy chain antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (56)..(56)  
; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that if Xaa at position 57 is Ser or Thr, then Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn  
; OTHER INFORMATION: Thr, then Xaa at position 56 is not Asn  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (58)..(58)  
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at position 57 is Ser or Thr, then Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn  
; OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr  
PCT-US02-21323-21

Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160; Indels 0; Gaps 0;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALT 168  
Db 100 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 219  
Qy 229 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
Db 220 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 279  
Qy 289 HNAKTKPREEQYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPR 348  
Db 280 HNAKTKPREEQYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPR 339  
Qy 349 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
Db 340 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 442

RESULT 4  
PCT-US02-21324-21  
; Sequence 21, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14

Db 340 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 442

RESULT 3  
PCT-US02-21324-12  
; Sequence 12, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/313,576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/383,581  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: Humanized antibody 266 preferred heavy chain variable  
PCT-US02-21324-12

Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160; Indels 0; Gaps 0;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALT 168  
Db 100 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 219  
Qy 229 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
Db 220 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 279  
Qy 289 HNAKTKPREEQYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPR 348  
Db 280 HNAKTKPREEQYNSTYRVWSVLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPR 339  
Qy 349 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
Db 340 EPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 442

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; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/313, 221
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313, 224
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 12
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: HUMANIZED ANTIBODY HEAVY CHAIN
PCT-US02-26321-12

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220 ICPPCFAPPELLGGFSVFLEFPFNPRDILMISKIFEVICVVDDVSHEDEFVAFNWIVDGVEV 273

289 HNAKTPREEQNSTYRVVSVLTVLHDWLNQGEYKCKVSNKALPAPTEKTSIAKGQPR 348

[illegible]

349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 408

340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 399

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409 FLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK 451

b 400 FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442

## RESULT 6

CT-US02-26321-16

sequence 16, Application PC/TUS0226321  
GENERAL INFORMATION:

APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY

TITLE OF INVENTION: ASSAY METHOD FOR ALZHEIMER'S DISEASE  
FILE REFERENCE: 8792/292

CURRENT APPLICATION NUMBER: PCT/US02/26321

CURRENT FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: 50/224 087

PRIOR APPLICATION NUMBER: 00/334,987  
PRIOR FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 60/313,221

PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 60/313,224

PRIOR FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1

COLTARKE: TACCHETTI VESTITION 3.1  
SEQ ID NO 16

LENGTH: 442  
TYPE: DPT

LIFE: FRI  
ORGANISM: Artificial Sequence

**FEATURE:**

**OTHER INFORMATION:** Humanized Antibody

**FEATURE:**

NAME/KEY: MISC\_FEATURE

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; LOCATION: (1)..(442)
; OTHER INFORMATION: Humanized Antibody Heavy Chain
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (36)..(56)
; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that Xaa at position 57 is Ser or Thr
; OTHER INFORMATION: on 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr
; OTHER INFORMATION: , then Xaa at position 56 is not Asn
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)..(57)
; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that Xaa at
; OTHER INFORMATION: position 57 is Asn and Xaa at position 58 is Ser or Thr, then Xaa
; OTHER INFORMATION: position 57 is Asp or Pro
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (58)..(58)
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that Xaa at
; OTHER INFORMATION: position 56 is Asn and Xaa at position 57 is neither Asp nor Pro,
; OTHER INFORMATION: then Xaa at position 58 is neither Ser nor Thr
PCT-US02-26321-16
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Query Match 76.1%; Score 343; DB 1; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.4e-160;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168
Db 100 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 159

Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228
Db 160 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 219

Qy 229 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288
Db 220 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 279

Qy 289 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348
Db 280 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 339

Qy 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 408
Db 340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 399

Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451
Db 400 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 442
```

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RESULT 7
PCT-US02-11853-12
; Sequence 12, Application PC/TUS0211853
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X14958
; CURRENT APPLICATION NUMBER: PCT/US02/11853
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/287539
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized antibody
PCT-US02-11853-12

Query Match 76.1%; Score 343; DB 1; Length 449;
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Best Local Similarity 100.0%; Pred. No. 1.5e-160;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168
Db 107 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 166

Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228
Db 167 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 226

Qy 229 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288
Db 227 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 286

Qy 289 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348
Db 287 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 346

Qy 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 408
Db 347 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 406

Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451
Db 407 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 449
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RESULT 8
PCT-US02-11854A-12
; Sequence 12, Application PC/TUS0211854A
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: PCT/US02/11854A
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/287,653
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 453
; TYPE: PRT
; ORGANISM: humanized antibody
PCT-US02-11854A-12

Query Match 76.1%; Score 343; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.5e-160;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168
Db 111 DYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 170

Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228
Db 171 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 230

Qy 229 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288
Db 231 TCPCCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 290

Qy 289 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348
Db 291 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 350

Qy 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 408
Db 351 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF 410

Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451
Db 407 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451
```



Db 411 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

## RESULT 9

PCT-US02-11853-20  
; Sequence 20, Application PC/TUS0211853  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Humanized Antibodies  
; FILE REFERENCE: X14958  
; CURRENT APPLICATION NUMBER: PCT/US02/11853  
; CURRENT FILING DATE: 2002-04-26  
; PRIOR FILING DATE: 2002-04-26  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
PCT-US02-11853-20

Query Match 76.1%; Score 343; DB 1; Length 468;

Best Local Similarity 100.0%; Pred. No. 1.5e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	109	DYWGQGLTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT	168
Db	126	DYWGQGLTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT	185
Qy	169	SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKTH	228
Db	186	SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKTH	245
Qy	229	TCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV	288
Db	246	TCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV	305
Qy	289	HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	348
Db	306	HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	365
Qy	349	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	408
Db	366	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	425
Qy	409	FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451	
Db	426	FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 468	

## RESULT 10

PCT-US02-11854A-20  
; Sequence 20, Application PC/TUS0211854A  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Humanized Antibodies  
; FILE REFERENCE: X-14819  
; CURRENT APPLICATION NUMBER: PCT/US02/11854A  
; CURRENT FILING DATE: 2002-04-26  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 472  
; TYPE: PRT  
; ORGANISM: humanized antibody  
PCT-US02-11854A-20

Query Match 76.1%; Score 343; DB 1; Length 472;

Best Local Similarity 100.0%; Pred. No. 1.5e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	109	DYWGQGLTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT	168
Db	130	DYWGQGLTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALT	189
Qy	169	SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKTH	228
Db	190	SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSTKVDKKVEPKSCDKTH	249
Qy	229	TCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV	288
Db	250	TCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV	309
Qy	289	HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	348
Db	310	HNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR	369
Qy	349	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	408
Db	370	EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSF	429
Qy	409	FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451	
Db	430	FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 472	

## RESULT 11

US-10-206-008-636  
; Sequence 636, Application US/10206008  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT253CIN  
; CURRENT APPLICATION NUMBER: US/10/206,008  
; CURRENT FILING DATE: 2002-07-29  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-08-14  
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; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-07-07  
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; PRIOR FILING DATE: 2000-08-14  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR FILING DATE: 2000-09-27

1	PRIOR FILING DATE: 2000-11-08	
2	PRIOR APPLICATION NUMBER: 60/249,216	
3	PRIOR FILING DATE: 2000-11-17	
4	PRIOR APPLICATION NUMBER: 60/249,210	
5	PRIOR FILING DATE: 2000-11-17	
6	PRIOR APPLICATION NUMBER: 60/226,681	
7	PRIOR FILING DATE: 2000-08-22	
8	PRIOR APPLICATION NUMBER: 60/225,759	
9	PRIOR FILING DATE: 2000-08-14	
10	PRIOR APPLICATION NUMBER: 60/225,213	
11	PRIOR FILING DATE: 2000-08-14	
12	PRIOR APPLICATION NUMBER: 60/227,182	
13	PRIOR FILING DATE: 2000-08-22	
14	PRIOR APPLICATION NUMBER: 60/225,214	
15	PRIOR FILING DATE: 2000-08-14	
16	PRIOR APPLICATION NUMBER: 60/235,836	
17	PRIOR FILING DATE: 2000-09-27	
18	PRIOR APPLICATION NUMBER: 60/230,438	
19	PRIOR FILING DATE: 2000-09-06	
20	PRIOR APPLICATION NUMBER: 60/215,135	
21	PRIOR FILING DATE: 2000-06-30	
22	PRIOR APPLICATION NUMBER: 60/225,266	
23	PRIOR FILING DATE: 2000-08-14	
24	PRIOR APPLICATION NUMBER: 60/249,218	
25	PRIOR FILING DATE: 2000-11-17	
26	PRIOR APPLICATION NUMBER: 60/249,208	
27	PRIOR FILING DATE: 2000-11-17	
28	PRIOR APPLICATION NUMBER: 60/249,213	
29	PRIOR FILING DATE: 2000-11-17	
30	PRIOR APPLICATION NUMBER: 60/249,212	
31	PRIOR FILING DATE: 2000-11-17	
32	PRIOR APPLICATION NUMBER: 60/249,207	
33	PRIOR FILING DATE: 2000-11-17	
34	PRIOR APPLICATION NUMBER: 60/249,245	
35	PRIOR FILING DATE: 2000-11-17	
36	PRIOR APPLICATION NUMBER: 60/249,244	
37	PRIOR FILING DATE: 2000-11-17	
38	PRIOR APPLICATION NUMBER: 60/249,217	
39	PRIOR FILING DATE: 2000-11-17	
40	PRIOR APPLICATION NUMBER: 60/249,211	
41	PRIOR FILING DATE: 2000-11-17	
42	PRIOR APPLICATION NUMBER: 60/249,215	
43	PRIOR FILING DATE: 2000-11-17	
44	PRIOR APPLICATION NUMBER: 60/249,264	
45	PRIOR FILING DATE: 2000-11-17	
46	PRIOR APPLICATION NUMBER: 60/249,214	
47	PRIOR FILING DATE: 2000-11-17	
48	PRIOR APPLICATION NUMBER: 60/249,297	
49	PRIOR FILING DATE: 2000-11-17	
50	PRIOR APPLICATION NUMBER: 60/232,400	
51	PRIOR FILING DATE: 2000-09-14	
52	PRIOR APPLICATION NUMBER: 60/231,242	
53	PRIOR FILING DATE: 2000-09-08	
54	PRIOR APPLICATION NUMBER: 60/232,081	
55	PRIOR FILING DATE: 2000-09-08	
56	PRIOR APPLICATION NUMBER: 60/232,080	
57	PRIOR FILING DATE: 2000-09-08	
58	PRIOR APPLICATION NUMBER: 60/231,414	
59	PRIOR FILING DATE: 2000-09-08	
60	PRIOR APPLICATION NUMBER: 60/231,244	
61	PRIOR FILING DATE: 2000-09-08	
62	PRIOR APPLICATION NUMBER: 60/233,064	
63	PRIOR FILING DATE: 2000-09-14	
64	PRIOR APPLICATION NUMBER: 60/233,063	
65	PRIOR FILING DATE: 2000-09-14	
66	PRIOR APPLICATION NUMBER: 60/232,397	
67	PRIOR FILING DATE: 2000-09-14	
68	PRIOR APPLICATION NUMBER: 60/232,399	
69	PRIOR FILING DATE: 2000-09-14	
70	PRIOR APPLICATION NUMBER: 60/232,401	
71	PRIOR FILING DATE: 2000-09-14	
72	PRIOR APPLICATION NUMBER: 60/241,808	
73	PRIOR FILING DATE: 2000-10-20	

; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 76.1%; Score 343; DB 6; Length 494;  
Best Local Similarity 100.0%; Pred. No. 1.5e-160; Indels 0; Gaps 0;  
Matches 343; Conservative 0; Mismatches 0;  
QY 109 DWGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 168  
DB 152 DWGQGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 211  
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 228  
DB 212 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 271  
QY 229 TCPGPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
DB 272 TCPGPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 331  
QY 289 HNAKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 348  
DB 332 HNAKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 391  
QY 349 EQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
DB 392 EQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 451  
QY 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 451  
DB 452 FLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 494

RESULT 12  
PCT-US02-21281-18  
; Sequence 18, Application PC/TUS0221281  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Interleukin-1 Beta Antibodies  
; FILE REFERENCE: X-14900  
; CURRENT APPLICATION NUMBER: PCT/US02/21281  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: US 60/307,973  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: US 60/312,278  
; PRIOR FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: patent in version 3.1  
; SEQ ID NO 18  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody full-length heavy chain region  
PCT-US02-21281-18

Query Match 75.8%; Score 342; DB 1; Length 450;  
Best Local Similarity 100.0%; Pred. No. 4.5e-160; Indels 0; Gaps 0;  
Matches 342; Conservative 0; Mismatches 0;  
QY 110 YMQGGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 169  
DB 109 YMQGGLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 168  
QY 170 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 229

DB 169 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 228  
QY 230 CPCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 289  
DB 229 CPCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
QY 290 NAKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 349  
DB 289 NAKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 348  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
DB 349 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 451  
DB 409 LYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 450

RESULT 13  
PCT-US01-27352-2  
; Sequence 2, Application PC/TUS0127352  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND  
; FILE REFERENCE: A0966PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/27352  
; CURRENT FILING DATE: 2002-08-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: humanized 5c8 heavy chain amino acid  
PCT-US01-27352-2

Query Match 75.6%; Score 341; DB 1; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.4e-159; Indels 0; Gaps 0;  
Matches 341; Conservative 0; Mismatches 0;  
QY 111 WQGGTLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 170  
DB 108 WQGGTLTVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNMNGALT 167  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 230  
DB 168 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH 227  
QY 231 CPCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 290  
DB 228 CPCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 287  
QY 291 AKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 350  
DB 288 AKTKPREEQYNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPR 347  
QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 410  
DB 348 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 407  
QY 411 YSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 451  
DB 408 YSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 448

RESULT 14  
US-09-791-118977  
; Sequence 118977, Application US/09791537

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; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118977
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-118977

Query Match 75.6%; Score 341; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.4e-159;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVPVTVSWNSGALTSG 170
DB 133 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVPVTVSWNSGALTSG 192

QY 171 VHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 230
DB 193 VHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 252

QY 231 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
DB 253 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 312

QY 291 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 350
DB 313 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 372

QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 410
DB 373 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 432

QY 411 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 451
DB 433 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 473

RESULT 15
US-09-791-537-104528
; Sequence 104528, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104528
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-104528

Query Match 75.6%; Score 341; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-159;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVPVTVSWNSGALTSG 170
DB 136 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVPVTVSWNSGALTSG 195
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QY 171 VHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 230
DB 196 VHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 255
QY 231 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
DB 256 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 315
QY 291 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 350
DB 316 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 375
QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 410
DB 376 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 435
QY 411 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 451
DB 436 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 476
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Search completed: October 9, 2002, 19:33:56  
Job time : 60.8265 secs

Gencore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:19:35 ; Search time 24.1607 seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	73.2	330	1 GHU	Ig gamma-1 chain C
2	230	51.0	255	4 S31866	Ig gamma-1 chain C
3	153	33.9	234	2 PT0207	Ig gamma chain C r
4	140	31.0	374	2 S69339	Ig heavy chain V r
5	109	24.2	220	2 A49444	Ig gamma-1 heavy C
6	90	20.0	218	2 A36040	Ig heavy chain V-I
7	89	19.7	249	2 S69340	Ig heavy chain VHI
8	65	14.4	377	2 A60764	Ig gamma-3 chain C
9	65	14.4	377	2 A23511	Ig gamma-3 chain C
10	63	14.0	120	2 S36278	Ig heavy chain V r
11	62	13.7	97	2 S26652	Ig gamma-1 chain C
12	57	12.6	327	1 G4HU	Ig gamma-4 chain C
13	53	11.8	241	2 S69131	Ig heavy chain (DO
14	53	11.8	326	1 G2HU	Ig gamma-2 chain C
15	51	11.3	90	2 S24248	Ig heavy chain V r
16	48	10.6	98	2 S26889	Ig heavy chain V r
17	48	10.6	99	2 S24259	Ig heavy chain V r
18	48	10.6	100	2 S24258	Ig heavy chain V r
19	48	10.6	101	2 S24257	Ig heavy chain V r
20	48	10.6	102	2 S24260	Ig heavy chain V r
21	48	10.6	104	2 S24255	Ig heavy chain V r
22	48	10.6	106	2 S24256	Ig heavy chain V r
23	48	10.6	108	2 PH1648	Ig heavy chain V r
24	48	10.6	109	2 PH1649	Ig heavy chain V r
25	48	10.6	112	2 PH1647	Ig heavy chain V r
26	48	10.6	117	2 A45953	Ig heavy chain pre
27	48	10.6	118	2 S31121	Ig heavy chain - h
28	48	10.6	119	2 S36005	Ig heavy chain V r
29	48	10.6	119	2 D36005	Ig heavy chain V r

#### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C:Accession: A93433; S33887; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S33861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the G1m(non-I) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

Ig heavy chain - h  
Ig heavy chain - h  
Ig heavy chain V r  
Ig heavy chain - h  
Ig heavy chain - h  
Ig heavy chain V r  
Ig heavy chain pre  
Ig heavy chain V r  
Ig heavy chain - h  
Ig heavy chain - h  
Ig gamma-3 heavy c  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain pre  
Ig heavy chain pre

igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 270-281, 'D', 283-306, 'K', 308-319, 'D', 321-330, 'D', 332-343, 'D', 345-356, 'K', 358-369, 'D', 371-382, 'D', 384-395, 'D', 397-408, 'D', 410-421, 'D', 423-434, 'D', 436-447, 'D', 449-460, 'D', 462-473, 'D', 475-486, 'D', 488-499, 'D', 501-512, 'D', 514-525, 'D', 527-538, 'D', 540-551, 'D', 553-564, 'D', 566-577, 'D', 579-590, 'D', 592-603, 'D', 605-616, 'D', 618-629, 'D', 631-642, 'D', 644-655, 'D', 657-668, 'D', 670-681, 'D', 683-694, 'D', 696-707, 'D', 709-720, 'D', 722-733, 'D', 735-746, 'D', 748-759, 'D', 761-772, 'D', 774-785, 'D', 787-798, 'D', 800-811, 'D', 813-824, 'D', 826-837, 'D', 839-850, 'D', 852-863, 'D', 865-876, 'D', 878-889, 'D', 891-902, 'D', 904-915, 'D', 917-928, 'D', 930-941, 'D', 943-954, 'D', 956-967, 'D', 969-980, 'D', 982-993, 'D', 995-1006, 'D', 1008-1019, 'D', 1021-1032, 'D', 1034-1045, 'D', 1047-1058, 'D', 1060-1071, 'D', 1073-1084, 'D', 1086-1097, 'D', 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11417-11428, 'D', 11430-11441, 'D', 11443-11454, 'D', 11456-11467, 'D

## RESULT 4

S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687  
A:Accession: S69339  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140/'C'/142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 31.0%; Score 140; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4.le-125;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 EPKSCDKTCTCPAPPELLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKF 279

Db 143 EPKSCDKTCTCPAPPELLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKF 202

QY 280 NWTVDGVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIETK 339

Db 203 NWTVDGVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIETK 262

QY 340 ISKAKGQPREPOVYITLPPSR 359

Db 263 ISKAKGQPREPOVYITLPPSR 282

## RESULT 5

A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
C:Accession: A49444  
R:Saul, F.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A resolution  
A:Reference number: A49444; MUID:93066153  
A:Accession: A49444  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-220 <SAU>  
A:Note: sequence modified after extraction from NCBI backbone  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;137-202/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 109; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 8.6e-96;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFP 175

Db 112 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHTFP 171

QY 176 AVLQSSGLYSLSSVTPSPSSILGTOTYICNVNHNKPSNTKVDKVKPEKSC 224

|||||

Db 172 AVLQSSGLYSLSSVTPSPSSILGTOTYICNVNHNKPSNTKVDKVKPEKSC 220

## RESULT 6

A36040  
Ig heavy chain V-III region (ART) - human (fragments)  
C:Species: Homo sapiens (man)  
C>Date: 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 21-Jan-2000  
C:Accession: A36040  
R:Eulitz, M.; Weiss, D.T.; Solomon, A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6542-6546, 1990  
A:Title: Immunoglobulin heavy-chain-associated amyloidosis.  
A:Reference number: A36040; MUID:90370821  
A:Accession: A36040  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-218 <EUL>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;132-199/Domain: immunoglobulin homology <IMM>

Query Match 20.0%; Score 90; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.le-77;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GQPREQVYITLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 404

Db 113 GQPREQVYITLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 172

QY 405 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHE 434

Db 173 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHE 202

## RESULT 7

S69340  
Ig heavy chain VHIII-D-JH-CH3 region - human  
C:Species: Homo sapiens (man)  
C>Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: S69340  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687  
A:Accession: S69340  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-249 <KHA>  
A:Cross-references: EMBL:X81696  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F;162-229/Domain: immunoglobulin homology <IMM>

Query Match 19.7%; Score 89; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.le-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 422

Db 161 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 220

QY 423 QGNVFSCVMHEALHNHYTQKSLSLSPGK 451

Db 221 QGNVFSCVMHEALHNHYTQKSLSLSPGK 249

## RESULT 8

A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C>Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989

A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:90007613  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 65; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 1.1e-53;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 197  
Db 17 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 76

Qy 198 GTQTY 202  
Db 77 GTQTY 81

RESULT 9  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c  
A;Reference number: A23511; MUID:86148507  
A;Accession: A23511  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
C;Genetics:  
A;Gene: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 65; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 1.1e-53;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 197  
Db 17 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 76

Qy 198 GTQTY 202  
Db 77 GTQTY 81

RESULT 10  
S36278  
Ig heavy chain V region (clone alpha-PHY-23) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C;Accession: S36278  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36256; MUID:93178448  
A;Accession: S36278  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-120 <GRI>

A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:90007613  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 65; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 1.1e-53;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 197  
Db 17 STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSL 76

Qy 198 GTQTY 202  
Db 77 GTQTY 81

RESULT 10  
S36278  
Ig heavy chain V region (clone alpha-PHY-23) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C;Accession: S36278  
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A;Title: Human anti-self antibodies with high specificity from phage display libraries.  
A;Reference number: S36256; MUID:93178448  
A;Accession: S36278  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-120 <GRI>

A;Cross-references: EMBL:Z18830; NID:g33114; PIDN:CAA79282.1; PID:g939894  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 14.0%; Score 63; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.2e-52;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRAPCKGLEWISGSGSYIYADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVY 95  
Db 36 WVRAPCKGLEWISGSGSYIYADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVY 95

Qy 96 CAK 98  
Db 96 CAK 98

RESULT 11  
S26652  
Ig gamma-1 chain C region - chimpanzee (fragment)  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 20-Jun-2000  
C;Accession: S26652  
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybridomas 1, 23-26, 1990  
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies  
A;Reference number: S26652; MUID:91355693  
A;Accession: S26652  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-97 <EHR>  
C;Cross-references: EMBL:X65284; NID:g38236; PIDN:CAA46384.1; PID:gi333693  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 13.7%; Score 62; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.4e-51;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 ALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYIC 204  
Db 24 ALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYIC 83

Qy 205 NV 206  
Db 84 NV 85

RESULT 12  
G4HU  
Ig gamma-4 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C;Accession: A90933; A90249; A02150  
R;Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A;Reference number: A90933; MUID:83157104  
A;Accession: A90933  
A;Molecule type: DNA  
A;Residues: 1-327 <ELL>  
A;Note: the sequence was determined from the germline gene  
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constan  
A;Reference number: A90249; MUID:70207360  
A;Accession: A90249  
A;Molecule type: protein  
A;Residues: 1-30;81-326 <PIN>  
C;Genetics:  
A;Gene: GDB:IGHG4



A:Cross-references: GDB:119340; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83/141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 57; DB 1; Length 327;  
Best Local Similarity 100.0%; Pred. No. 4e-46;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGT 199  
|||||  
DB 22 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGT 78  
|||||

RESULT 13  
S69131  
Ig heavy chain (DOT) - human (fragment)  
N:Alternate names: anti-riboflavin IgG Fd fragment  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000  
C:Accession: S69131  
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Perri, G.  
Eur. J. Biochem. 228, 886-893, 1995  
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins  
A:Reference number: S69130; MUID:95255298  
A:Accession: S69131  
A:Molecule type: protein  
A:Residues: 1-241 <STO>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid  
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MA>  
F:140-205/Domain: immunoglobulin homology <IMW>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 11.8%; Score 53; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 195  
|||||  
DB 142 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 194  
|||||

RESULT 14  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma chain components  
A:Reference number: A93906; MUID:82197621  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: GB:V00554; GB:J00230; NID:g323759; PID:CAB58438.1; PID:g6066056  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional analysis  
A:Reference number: A92809; MUID:81007873

A:Contents: myeloma protein T11  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, Q'21-57, Z', 59, A', 61-193, D', 195-325 <WAN>  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of human immunoglobulin G2  
A:Reference number: A90752; MUID:80001357  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, E', 26-57, EV', 60-85, 132-171, Z'22', 175, B', 177-193, D', 195-196, Q', 1  
A:Note: This sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G2  
A:Reference number: A93132; MUID:80114419  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: The revised sequence differs from that shown in having 60-Ala and in the amidated  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83/140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.8%; Score 53; DB 1; Length 326;  
Best Local Similarity 100.0%; Pred. No. 2.6e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 195  
|||||  
DB 22 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 74  
|||||

RESULT 15  
S24248  
Ig heavy chain V region (VH26) - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S24248  
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
submitted to the EMBL Data Library, June 1992  
A:Description: A single VH gene predominates in the rearranged and expressed human B cell repertoire  
A:Reference number: S24247

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A:Accession: S24248  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-90 <STEP>  
A:Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA7454.1; PID:g38396  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 11.3%; Score 51; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 6.8e-41;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 PGKLEWVSGISGGSGTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDT 91  
 |||||  
 Db 40 PGKLEWVSGISGGSGTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDT 90

Search completed: October 9, 2002, 19:25:52  
Job time : 24.1607 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:13:25 ; Search time 13.8061 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALHNYTKSLSLSPGK 451

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	73.2	330	1 GCI_HUMAN	P01857 homo sapien
2	57	12.6	327	1 GC4_HUMAN	P01861 homo sapien
3	53	11.8	326	1 GC2_HUMAN	P01859 homo sapien
4	45	10.0	290	1 GC3_HUMAN	P01860 homo sapien
5	44	9.8	116	1 HV05_CARAU	P19181 carassius a
6	37	8.2	117	1 HV3C_HUMAN	P01784 homo sapien
7	25	5.5	323	1 GC_RABIT	P01870 oryctolagus
8	23	5.1	113	1 HV3D_HUMAN	P01785 homo sapien
9	23	5.1	116	1 HV3R_HUMAN	P01779 homo sapien
10	23	5.1	119	1 HV3M_HUMAN	P01774 homo sapien
11	23	5.1	119	1 HV3N_HUMAN	P01775 homo sapien
12	23	5.1	119	1 HV3P_HUMAN	P01777 homo sapien
13	23	5.1	120	1 HV3E_HUMAN	P01766 homo sapien
14	21	4.7	117	1 HV3Q_HUMAN	P01776 homo sapien
15	20	4.4	126	1 HV01_CANEA	P01772 homo sapien
16	19	4.2	114	1 HV3K_HUMAN	P01784 canis famli
17	19	4.2	329	1 GC2_CAVPO	P01862 cavia porce
18	17	3.8	117	1 HV17_MOUSE	P01786 mus musculu
19	17	3.8	122	1 HV20_MOUSE	P01789 mus musculu
20	17	3.8	122	1 HV21_MOUSE	P01790 mus musculu
21	17	3.8	123	1 HV18_MOUSE	P01787 mus musculu
22	17	3.8	123	1 HV19_MOUSE	P01788 mus musculu
23	17	3.8	123	1 HV22_MOUSE	P01791 mus musculu
24	17	3.8	123	1 HV23_MOUSE	P01792 mus musculu
25	17	3.8	123	1 HV24_MOUSE	P01793 mus musculu
26	17	3.8	123	1 HV25_MOUSE	P01794 mus musculu
27	17	3.8	144	1 HV26_MOUSE	P01795 mus musculu
28	16	3.5	115	1 HV3F_HUMAN	P01767 homo sapien
29	16	3.5	115	1 HV3S_HUMAN	P01780 homo sapien
30	16	3.5	122	1 HV3A_HUMAN	P01762 homo sapien
31	15	3.3	121	1 HV3J_HUMAN	P01771 homo sapien
32	14	3.1	114	1 HV3B_HUMAN	P01763 homo sapien
33	14	3.1	116	1 HV1A_RABIT	P01826 oryctolagus

34	14	3.1	117	1 HV03_CARAU	P19180 carassius a
35	13	2.9	97	1 HV56_MOUSE	P18527 mus musculu
36	13	2.9	98	1 HV57_MOUSE	P18528 mus musculu
37	13	2.9	116	1 HV3Q_HUMAN	P01778 homo sapien
38	13	2.9	116	1 HV3T_HUMAN	P01781 homo sapien
39	13	2.9	117	1 HV58_MOUSE	P18529 mus musculu
40	13	2.9	117	1 HV59_MOUSE	P18530 mus musculu
41	13	2.9	118	1 HV3V_HUMAN	P80419 homo sapien
42	13	2.9	119	1 HV3I_HUMAN	P01770 homo sapien
43	13	2.9	122	1 HV3G_HUMAN	P01768 homo sapien
44	13	2.9	124	1 HV01_HUMAN	P01760 homo sapien
45	13	2.9	142	1 HV01_RAT	P01805 rattus norv

#### ALIGNMENTS

RESULT 1  
GCI\_HUMAN  
ID GCI\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN IGHG1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE  
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
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 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
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 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC RESIDUES 198, 267 & 272.  
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 CC -----  
 DR EMBL; J00228; AAC84527.1; ALT\_INIT.  
 DR PIR; A02146; GHRI.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR MIM; 147100; -.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
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 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW 3D-structure.  
 FT NON\_TER 1 1  
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 FT DISULFID 27 83  
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 DB 181 STYRVSVLTIVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
 QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 421  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
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 DB 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
 RESULT 2  
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 ID GC4\_HUMAN STANDARD; PRT; 327 AA.  
 AC P01861;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-4 chain C region.  
 OS IGHG4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
  constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
  heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
  genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
  evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
  domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
  immunoglobulin gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RT Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
  immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
RN [11]
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DR HSSP; P01842; 7FAB.
DR MM; 147130; -.
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DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
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DR SMART; SM00407; IGc1; 2.
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FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
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FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201 INTERCHAIN (WITH A HEAVY CHAIN).
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D D 22 TAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGT 78
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AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RA Ellison J.W., Hood L.E.;
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FT /FTid=VAR_003893.
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FT /FTid=VAR_003895.
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Db 72 CPAPELLGGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEV 116

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ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Last Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
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FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT NON_TER 117 117
FT NCBI_TaxID=7957;
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 9.8%; Score 44; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2,1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 72 SGGSTYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYICA 115

RESULT 6
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AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
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DR InterPro; IPR003596; Ig_V.
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DR SMART; SM00406; IGV; 1.
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Db 81 DSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYCAK 117

RESULT 7
ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Moie L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349(1975).
RN [3]

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RP SEQUENCE OF 88-266 FROM N.A.  
RX MEDLINE=8329917; PubMed=6193512;  
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
heavy chain and identification of two genomic C gamma genes.";   
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
RN [4]  
RP SEQUENCE OF 132-161.  
RX MEDLINE=70110015; PubMed=5461106;  
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
RT "Sequence studies of the Fd section of the heavy chain of rabbit  
immunoglobulin G.";   
RL Biochem. J. 116:249-259(1970).  
RN [5]  
RP SEQUENCE OF 129-131 AND 155-322.  
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
RL (In) Killander J. (eds.);  
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
Stockholm (1967).  
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
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MARKERS AND REF.5 THE E15 MARKER.  
CC -----  
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CC -----  
CC EMBL; M16426; AAA31289.1; -.  
DR PIR; A02161; GHRB.  
DR HSSP; P01857; 1FC1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGCL; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT VARIANT 104 104 T -> M (IN D11 MARKER).  
FT VARIANT 185 185 T -> A (IN E15 MARKER).  
FT CONFLICT 48 48 N -> E (IN REF. 2).  
FT CONFLICT 71 71 V -> VPV (IN REF. 2).  
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).  
FT CONFLICT 173 173 N -> D (IN REF. 5).  
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).  
FT CONFLICT 201 201 N -> D (IN REF. 5).  
FT CONFLICT 218 218 Q -> E (IN REF. 5).  
FT CONFLICT 233 233 E -> Q (IN REF. 5).  
FT CONFLICT 246 246 N -> D (IN REF. 5).  
FT CONFLICT 256 256 E -> G (IN REF. 5).  
FT CONFLICT 260 260 N -> D (IN REF. 5).  
FT CONFLICT 266 266 N -> D (IN REF. 5).  
FT CONFLICT 280 280 Y -> W (IN REF. 5).  
FT CONFLICT 284 284 N -> S (IN REF. 5).  
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;  
  
Query Match 5.5%; Score 25; DB 1; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 247 FPPKPKDTLMISRTPEVTCVVVDVS 271  
Db 119 FPPKPKDTLMISRTPEVTCVVVDVS 143  
|||||  
  
RESULT 8  
HV3D\_HUMAN STANDARD; PRT; 115 AA.  
ID HV3D\_HUMAN  
AC P01765;  
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-III region TIL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=78005528; PubMed=409716;  
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;  
RT "Immunoglobulin structure and genetics. Identity between variable  
regions of a mu and a gamma2 chain.";   
RL J. Biol. Chem. 252:7192-7199(1977).  
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS  
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL  
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO  
IDENTICAL.  
DR PIR; A02048; H3HUTL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
KW Immunoglobulin V region.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;  
  
Query Match 5.1%; Score 23; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.4e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SGGGLVQPGGSLRLSCAASGFTF 29  
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29  
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RESULT 9  
HV3D\_HUMAN STANDARD; PRT; 116 AA.  
ID HV3D\_HUMAN  
AC P01779;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-III region TUR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=74142702; PubMed=4522793;  
RA Capra J.D., Kehoe J.M.;  
RT "Variable region sequences of five human immunoglobulin heavy chains  
of the VH3 subgroup: definitive identification of four heavy chain  
hypervariable regions.";   
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGAL MYELOMA  
PROTEIN.  
DR PIR; A02062; ALHUTU.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
KW Immunoglobulin V region.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12431 MW; EB705F53A963F0C CRC64;  
  
Query Match 5.1%; Score 23; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 6.5e-16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SGGGLVQPGGSLRLSCAASGFTF 29  
|||||



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Db      7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 10
HV3M_HUMAN
ID      HV3M_HUMAN      STANDARD;      PRT;      119 AA.
AC      P01774;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V-III region POM.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=75046755; PubMed=4139708;
RA      Capra J.D., Kehoe J.M.;
RT      "Structure of antibodies with shared idiotypic: the complete sequence
RT      of the heavy chain variable regions of two immunoglobulin M
RT      anti-gamma globulins.";
RL      Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC      -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC      GLOBULIN ACTIVITY.
DR      PIR; A02057; M3HUPM.
DR      HSSP; P01772; 2IG2.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
KW      Immunoglobulin V region.
FT      VARIANT      54      54
FT      NON_TER      119      119
SQ      SEQUENCE      119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;

Query Match      5.1%; Score 23; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 SGGGLVQPGGSLRLSCAASGFTF 29
Db      7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 11
HV3N_HUMAN
ID      HV3N_HUMAN      STANDARD;      PRT;      119 AA.
AC      P01775;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V-III region LAY.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=75046755; PubMed=4139708;
RA      Capra J.D., Kehoe J.M.;
RT      "Structure of antibodies with shared idiotypic: the complete sequence
RT      of the heavy chain variable regions of two immunoglobulin M
RT      anti-gamma globulins.";
RL      Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC      -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC      GLOBULIN ACTIVITY.
DR      PIR; A02058; M3HULY.
DR      HSSP; P01772; 2IG2.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.

Db      7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 12
HV3P_HUMAN
ID      HV3P_HUMAN      STANDARD;      PRT;      119 AA.
AC      P01777;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V-III region TEI.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=74142702; PubMed=4522793;
RA      Capra J.D., Kehoe J.M.;
RT      "Variable region sequences of five human immunoglobulin heavy chains
RT      of the VH3 subgroup: definitive identification of four heavy chain
RT      hypervariable regions.";
RL      Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC      -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGS1 MYELOMA
CC      PROTEIN.
DR      PIR; A02060; G1HUTE.
DR      HSSP; P01772; 2IG2.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
KW      Immunoglobulin V region.
FT      NON_TER      119      119
SQ      SEQUENCE      119 AA; 13802 MW; 7E24DC852C7290A9 CRC64;

Query Match      5.1%; Score 23; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 SGGGLVQPGGSLRLSCAASGFTF 29
Db      7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 13
HV3E_HUMAN
ID      HV3E_HUMAN      STANDARD;      PRT;      120 AA.
AC      P01766;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V-III region BRO.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=77117674; PubMed=65324;
RA      Capra J.D., Hopper J.E.;
RT      "Comparative studies on monotypic IgM lambda and IgG kappa from an

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RT individual patient. III. The complete amino acid sequence of the VH
RL region of the IgM paraprotein.;
CC Immunohistochemistry 13:995-999(1976).
CC -)- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
DR PIR: A02049; M3HUBW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2B6410 CRC64;

Query Match 5.1%; Score 23; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGGGLVQPGGSLRLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29

RESULT 14
HV30_HUMAN STANDARD; PRT; 117 AA.
AC P01776;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region WAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -)- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR: A02059; GIHWS.
DR HSSP; P01772; 2IG2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13091 MW; 201DEF0E1E53D9BF CRC64;

Query Match 4.7%; Score 21; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGGGLVQPGGSLRLSCAASGF 27
Db 7 SGGGLVQPGGSLRLSCAASGF 27

RESULT 15
HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region KOL.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
DR PIR: A02055; GIHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 4.4%; Score 20; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 YADSVKGRFTISRDNKNTL 79
Db 60 YADSVKGRFTISRDNKNTL 79

Search completed: October 9, 2002, 19:23:37
Job time : 13.8061 secs
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 38.5421 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	232	51.4	701	Q96PQ8	Q96PQ8 homo sapien
2	40	8.9	113	Q9UL90	Q9UL90 homo sapien
3	38	8.4	112	Q9UGP3	Q9UGP3 homo sapien
4	35	7.8	147	Q9V509	Q9V509 homo sapien
5	34	7.5	116	Q9UL93	Q9UL93 homo sapien
6	34	7.5	118	Q9UL72	Q9UL72 homo sapien
7	25	5.5	597	Q96BB9	Q96BB9 homo sapien
8	23	5.1	95	Q9ULB6	Q9ULB6 homo sapien
9	23	5.1	118	Q9UL91	Q9UL91 homo sapien
10	23	5.1	121	Q9UL71	Q9UL71 homo sapien
11	19	4.2	112	Q9HCC1	Q9HCC1 homo sapien
12	18	4.0	122	Q9UL84	Q9UL84 homo sapien
13	17	3.8	104	Q9UL87	Q9UL87 homo sapien
14	16	3.5	131	Q9UL88	Q9UL88 homo sapien
15	16	3.5	150	Q9Y298	Q9Y298 homo sapien
16	16	3.5	496	Q96KX8	Q96KX8 homo sapien

17	15	3.3	384	4	Q9UP60	Q9UP60 homo sapien
18	14	3.1	480	11	Q9IXE1	Q9IXE1 mus musculu
19	14	3.1	494	4	Q96K68	Q96K68 homo sapien
20	13	2.9	119	4	Q9UL73	Q9UL73 homo sapien
21	13	2.9	119	11	Q920E7	Q920E7 mus musculu
22	13	2.9	121	4	Q9UL96	Q9UL96 homo sapien
23	13	2.9	122	4	Q9UL75	Q9UL75 homo sapien
24	13	2.9	124	4	Q9UL92	Q9UL92 homo sapien
25	13	2.9	337	6	Q95M34	Q95M34 equus cabal
26	13	2.9	496	4	Q96DK0	Q96DK0 mus musculu
27	12	2.7	124	6	Q9N0W6	Q9N0W6 oryctolagus
28	12	2.7	124	6	Q9N0W4	Q9N0W4 oryctolagus
29	12	2.7	157	4	Q95978	Q95978 homo sapien
30	12	2.7	298	11	Q9QVF0	Q9QVF0 mus musculu
31	12	2.7	437	11	Q9RIA4	Q9RIA4 mus musculu
32	12	2.7	463	11	Q9LIC4	Q9LIC4 mus musculu
33	12	2.7	468	11	Q9L31	Q9L31 mus musculu
34	12	2.7	473	11	Q9L25	Q9L25 mus musculu
35	12	2.7	488	11	Q9LWR1	Q9LWR1 mus musculu
36	12	2.7	613	4	Q96EY0	Q96EY0 mus musculu
37	11	2.4	64	11	Q61750	Q61750 mus musculu
38	11	2.4	102	11	Q9JL79	Q9JL79 mus musculu
39	11	2.4	110	11	Q9JL83	Q9JL83 mus musculu
40	11	2.4	117	11	Q921C6	Q921C6 mus musculu
41	11	2.4	119	4	Q9UL94	Q9UL94 homo sapien
42	11	2.4	120	11	Q920E8	Q920E8 mus musculu
43	11	2.4	134	6	P83049	P83049 sus scrofa
44	11	2.4	139	11	Q924R5	Q924R5 mus musculu
45	11	2.4	473	11	Q9D8L4	Q9D8L4 mus musculu

#### ALIGNMENTS

##### RESULT 1

Q96PQ8 PRELIMINARY: PRT; 701 AA.  
 AC Q96PQ8;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21477448; PubMed=11593034;  
 RA Hu Z., Garen A.;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 DR EMBL; AF272774; AAK58686.1; .  
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 51.4%; Score 232; DB 4; Length 701;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-232;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 279  
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 DB 470 EPKSCDKHTCTCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 529  
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 QY 280 NMYVDGVEVHNKATKPREQNTSYRYVVSULTVLHQLNGKEYCKVSKNALPAPIEKT 339  
 |||||  
 DB 530 NMYVDGVEVHNKATKPREQNTSYRYVVSULTVLHQLNGKEYCKVSKNALPAPIEKT 589  
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 QY 340 ISKAKQPREPQVYITLPSRDELTKNQVSLTCLVKGYGSPIDIAVWESNGQPENNYKTPP 399  
 |||||  
 DB 590 ISKAKQPREPQVYITLPSRDELTKNQVSLTCLVKGYGSPIDIAVWESNGQPENNYKTPP 649  
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 QY 400 PVLDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

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|||||
Db 650 PVLDSGSEFLYSKTYDKSRWQGNFSCVMHEALHNHYTKQSLSPGK 701
|||||
RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
  (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match      8.9%; Score 40; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YVADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK 98
|||||
Db 59 YVADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK 98
|||||

RESULT 3
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN IGH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Zafiroopoulos A., Kandilogiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RA "Induction of somatic mutations in human B cells by in vitro
  immunization.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ122560; CAB65078.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;
```

```
Query Match      8.4%; Score 38; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA 97
|||||
Db 43 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCA 80
|||||

RESULT 4
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
  myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match      7.8%; Score 35; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 IDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG 142
|||||
Db 113 IDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG 147
|||||

RESULT 5
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
  (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
  fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 4; Length 116;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTA 92
DQ 58 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTA 91

RESULT 6
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003596; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 4; Length 118;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTA 92
DQ 58 YYADSVKGRFTISRDNKNTLYLQMNLSRAEDTA 91

RESULT 7
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOPHYSAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 25; DB 4; Length 597;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ISGSGGTYTADSVKGRFTISRDN 75
DQ 70 ISGSGGTYTADSVKGRFTISRDN 94

RESULT 8
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 9DA8C6D16D22574A CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 95;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
DQ 6 SGGGLVQPGGSLRLSCAASGFTF 28

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.
DR HSSP; P01772; 2FB4.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 5.1%; Score 23; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.6e-15; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 7 SGGGLVPGGSLRLSCAASGFTF 29
Db 7 SGGGLVPGGSLRLSCAASGFTF 29
|||||
RESULT 10
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 121
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 5.1%; Score 23; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-15; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 55 GGSYYVADSVKGRFTISRDN SKN 77
Db 55 GGSYYVADSVKGRFTISRDN SKN 77
|||||
RESULT 11
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme :isolation from a
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RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 112
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 4.2%; Score 19; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.1e-11; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 79 LYLQMNSLRAEDTAVYYCA 97
Db 79 LYLQMNSLRAEDTAVYYCA 97
|||||
RESULT 12
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 4.0%; Score 18; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.5e-10; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 81 LQMNSLRAEDTAVYYCAK 98
Db 81 LQMNSLRAEDTAVYYCAK 98
|||||
RESULT 13
Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
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DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035027; AAD56263.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 3.8%; Score 17; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWVSGIS 52
DB 15 WVRQAPGKGLEWVSGIS 31

RESULT 14
Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 3.5%; Score 16; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGGSLRLSCAASGFTF 29
DB 14 PGGSLRLSCAASGFTF 29

RESULT 15

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Q9Y298 PRELIMINARY; PRT; 150 AA.
ID Q9Y298;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Signal.
KW SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 3.5%; Score 16; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 VTVSSASTKGPSVFPL 132
DB 132 VTVSSASTKGPSVFPL 147

Search completed: October 9, 2002, 19:24:58
Job time : 39.5421 secs

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XX PS Claim 12; Page 106-108; 126pp; English.

XX CC The invention relates to an isolated tumour-associated antigen mucin-1

XX CC (MUC-1)-specific binding member comprising an antigen binding domain

XX CC region having an antibody variable light (VL) or heavy (VH) region,

XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

XX CC The binding of MUC1-specific binding member to MUC1 is detected by a

XX CC detection method selected from enzyme-linked immunosorbent assay,

XX CC magnetic resonance imaging, scintillation counting, and x-ray film.

XX CC MUC1-specific binding member is useful for treating cancer, preferably

XX CC adenocarcinoma, in an individual, where the cancer is present in tissue

XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

XX CC binding member is useful for diagnosing and imaging MUC1-expressing

XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,

XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

XX CC containing molecules, and for therapeutically or prophylactically

XX CC treating cancer. The present sequence is human recombinant immunoglobulin

XX CC (Ig) heavy chain region (variable VH and CH constant heavy chain).

XX SQ Sequence 451 AA;

Query Match 100.0%; Score 2411; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 5.2e-136;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120

DB 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180

DB 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180

QY 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPELLG 240

DB 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPELLG 240

QY 241 GPSVFLPPPKPDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300

DB 241 GPSVFLPPPKPDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300

QY 301 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

DB 301 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420

DB 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR 420

QY 421 WQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

DB 421 WQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

RESULT 2

AAV68810

ID AAV68810 standard; Protein; 449 AA.

XX AC AAV68810;

XX DT 16-MAY-2000 (first entry)

XX DE A rat heavy chain region and a human hinge region.

XX KW CD3 antigen complex; chimeric antibody; immunosuppression; heavy chain;

XX KW CD3 antigen-T-cell receptor complex; graft rejection; cancer.

OS Synthetic.

OS Rattus sp.

OS Homo sapiens.

XX WO200005268-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-GB02380.

XX 21-JUL-1998; 98GB-0015909.

XX (BTGI-) BTG INT LTD.

XX Waldmann H, Frewin M;

XX WPI; 2000-182655/16.

XX N-PSDB; AAZ60599.

XX New humanized anti-CD3 antibodies, used for treating cancer or for

XX immunosuppression and preventing graft rejection -

XX Disclosure; Page 45-47; 56pp; English.

XX The present sequence represents the heavy chain variable region of a rat

XX immunoglobulin G (IgG) antibody which is specific for the CD3 antigen

XX complex, and the human CH1-hinge-aglycosylCH2CH3. The specification

XX describes chimeric human/rodent anti-CD3 antibodies, which have a

XX rodent CD3 light chain variable region and a human heavy chain variable

XX region. The anti-CD3 antibodies can render T-cells non-functional by

XX antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex.

XX They can be used for immunosuppression, particularly for the control

XX of graft rejection. The antibodies can also enhance or re-direct T-cell

XX responses to antigens. They can be used in the treatment of cancer.

XX SQ Sequence 449 AA;

Query Match 94.2%; Score 2270; DB 21; Length 449;  
Best Local Similarity 94.9%; Pred. No. 1.3e-127;  
Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSFPMAVROAPGKGLVWVSTISTSGRTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAK--HTGGVWDPIDYWGQGLTV 117

DB 61 RVSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKFRQYSGG-----FDYWGQGLTV 115

QY 118 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177

DB 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175

QY 178 LOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPE 237

DB 176 LOSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPE 235

QY 238 LLGGPSVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297

DB 236 LLGGPSVFLFPPKPKDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295

QY 298 EOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 357

DB 296 EOYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 355

QY 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 417

DB 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 415

QY 418 KSRWQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

DB 416 KSRWQGGNVFSCSVMHREALNHHYTKQSLSPGK 449

```

RESULT 3
AAU07745 standard; Protein; 461 AA.
AC AAU07745;
DT 04-DEC-2001 (first entry)
DE Humanised monoclonal antibody Hu266, heavy chain.
KW Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
XX gene therapy.
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1..19
FT Peptide
FT /label= Signal_peptide
FT 20..461
FT /label= Mature_Hu266_heavy_chain
FT /note= "This sequence is specifically claimed in
FT claim 17"
XX
XX WO200162801-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-US06191.
XX
XX 24-FEB-2000; 2000US-0184601.
XX 08-DEC-2000; 2000US-0254465.
XX 08-DEC-2000; 2000US-0254498.
XX
XX (UNIW ) UNIV WASHINGTON.
XX (ELIL ) LILLY & CO ELI.
XX
XX Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
XX Vasquez N;
XX
XX WPT; 2001-550087/61.
XX
XX New humanised antibody for the treatment of Alzheimer's comprises the
XX inhibition and reduction of the formation of amyloid plaques -
XX
XX Example 13; Fig 5; 63pp; English.
XX
XX The invention relates a humanised antibody that specifically binds
XX an epitope contained within positions 13-28 of amyloid beta peptide,
XX Abeta. The antibody is useful to inhibit and reduce the formation of
XX amyloid plaques or the effects of toxic soluble Abeta species in humans
XX their fragments are used for the manufacture of a medicament. This includes
XX the prolonged expression of recombinant sequences of them in human
XX tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
XX Down's syndrome or pre clinical cerebral amyloid angiopathy.
XX Specifically, the antibody is used to sequester Abeta into plasma, brain
XX or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
XX peptide within the brain thereby improving cognition. The present
XX sequence is the heavy chain of a humanised monoclonal antibody, Hu266,
XX based on the mouse antibody 266.
XX
XX Sequence 461 AA;
XX
XX Query Match 92.8%; Score 2236.5; DB 22; Length 461;
XX Best Local Similarity 93.8%; Pred No. 1.3e-125;
XX Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;
XX
XX 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVWVQAPGKGLVWSGSGSTYY 60
XX :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
XX 20 EVQLVESGGGLVPGGSLRLSCAASGFTFRSRYSMVWVQAPGKGLVQINSVGNSTYY 79
XX

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QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120
DB 80 PDTVRGRTISRDNKNTLYLQMNLSRAEDTAVYYCAG-----DYWGQGLTVTVS 130
QY 121 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
DB 131 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 190
QY 181 SGYSLSSVTVTPSSSLGTQTVICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELIG 240
DB 191 SGYSLSSVTVTPSSSLGTQTVICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELIG 250
QY 241 GPSVFLEPPPKDKTLMISRTPEVTCVVYVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQY 300
DB 251 GPSVFLEPPPKDKTLMISRTPEVTCVVYVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQY 310
QY 301 NSTYRVVSVLTVLDHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
DB 311 NSTYRVVSVLTVLDHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 370
QY 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSR 420
DB 371 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSR 430
QY 421 WQGNVFSCSVMHREALNHNHYTKQSLSPGK 451
DB 431 WQGNVFSCSVMHREALNHNHYTKQSLSPGK 461

RESULT 4
AAU14288
ID AAU14288 standard; Protein; 477 AA.
AC AAU14288;
DT 24-OCT-2001 (first entry)
DE Human novel protein #159.
XX
XX Human; novel protein; Antianaemic; osteopathic; antinflammatory;
XX immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.
XX
XX Homo sapiens.
XX
XX WO200155437-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02623.
XX
XX 25-JAN-2000; 2000US-0491404.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-451939/48.
XX DR N-PSDB; AAS22593.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 611-612; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX

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CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicitor an immune response, and to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host diseases, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.

XX SQ Sequence 477 AA;

Query Match 92.5%; Score 2229.5; DB 22; Length 477;  
Best Local Similarity 91.5%; Pred. No. 3.6e-125; Indels 13; Gaps 2;  
Matches 422; Conservative 10; Mismatches 16;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60  
DB 20 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 79  
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDP-----IDY 110  
DB 80 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDP-----IDY 136  
QY 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSG 170  
DB 137 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSG 196  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTRKVDKVKPKSCDKTHTC 230  
DB 197 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTRKVDKVKPKSCDKTHTC 256  
QY 231 PPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
DB 257 PPCPAPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 316  
QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREP 350  
DB 317 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREP 376  
QY 351 QVTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPL 410  
DB 377 QVTLPPSDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPL 436  
QY 411 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
DB 437 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 477

RESULT 5

AAR20057 standard; Protein: 475 AA.

XX AC AAR20057;

XX DT 25-MAR-1992 (first entry)

XX DE Heavy chain of 3D6 anti-HIV antibody.

XX KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;

complementarity determining region.  
KW XX Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Region 20..49  
FT /label= signal  
FT /label= Framework\_1  
FT Region 50..54  
FT /label= CDR-1  
FT Region 55..68  
FT /label= Framework\_2  
FT Region 69..85  
FT /label= CDR\_2  
FT Region 86..117  
FT /label= Framework\_3  
FT Region 118..134  
FT /label= CDR\_3  
FT Region 135..145  
FT /label= Framework\_4  
FT Region 146..175  
FT /label= Constant\_region  
XX XX W09118983-A.  
XX PD 12-DEC-1991.  
XX PF 28-MAY-1991; 91WO-1000067.  
XX PR 29-MAY-1990; 90AT-0001178.  
XX PA (JUNG/) JUNGBAUER A.  
PI Reigenhauer M, Himmeler G, Kohl J, Steindl F;  
DR WPI; 1992-007468/01.  
DR N-PSDB; AAQ20066.  
XX XX Recombinant protein which binds to complex viral antigen and  
PT HIV-1 - contains variable region of antibody derived from 3D6  
PT cell line, used for detecting HIV-1 antigen  
XX XX Claim 2; Page 24; 52pp; German.  
CC The variable region of the heavy chain is used in a recombinant  
CC protein which the variable region from the kappa light chain of 3D6,  
CC the two V regions being joined by a linker. The recombinant protein  
CC binds to HIV gp160.  
CC See also AAQ20067 and AAQ20068.  
XX XX Sequence 475 AA;

Query Match 92.4%; Score 2228.5; DB 13; Length 475;  
Best Local Similarity 92.8%; Pred. No. 4.1e-125; Indels 5; Gaps 1;  
Matches 423; Conservative 7; Mismatches 21;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 79  
QY 61 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGT 115  
DB 80 ADSVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGT 139  
QY 116 LVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 175  
DB 140 LVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 199  
QY 176 AVQLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTRKVDKVKPKSCDKTHTCPCPA 235  
DB 200 AVQLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTRKVDKVKPKSCDKTHTCPCPA 259

QY 236 PELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 295  
 DB 260 PELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 319  
 QY 296 REEQYNSYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTL 355  
 DB 320 REEQYNSYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTL 379  
 QY 356 PPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLT 415  
 DB 380 PPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLT 439  
 QY 416 VDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 451  
 DB 440 VDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 475

RESULT 6  
 AAB81987  
 ID AAB81987 standard; Protein: 582 AA.  
 XX  
 AC AAB81987;  
 DT 03-JUL-2001 (first entry)  
 XX  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
 XX  
 KW Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WC200123432-A1.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 29-SEP-2000; 2000WO-JP06774.  
 XX  
 PR 30-SEP-1999; 99JP-0278291.  
 PR 06-APR-2000; 2000JP-0105088.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Hanai N, Shitara K, Nakamura K, Niwa R;  
 XX  
 DR WPI; 2001-266143/27.  
 XX  
 XX New human type complementation-determining region-transplanted antibody  
 PT and derivatives against ganglioside GD3, useful in diagnosis and  
 PT therapy of e.g. tumours, with low antigenicity, little side effects but  
 PT potent activity in cancer -  
 XX  
 PS Claim 41; Page 168-172; 183pp; Japanese.  
 XX  
 CC The present invention describes a monoclonal antibody which can react  
 CC specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 582 AA;  
 Query Match 91.9%; Score 2216; DB 22; Length 582;  
 Best Local Similarity 92.7%; Pred. No. 2.8e-124;  
 Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;  
 QY 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFRSNAMGWTRQAPGKLEWVSIGSGGSTYY 60  
 DB 1 EVQLVESGGDFVQPGSLRLVCAASGFAFSHYAMSWVRQAPGKLEWVAIISGGSGSTYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYCAKHTGGGVWDPIYWGQGTLLVTVS 120  
 DB 61 SDSVKGRFTISRDNKNTLYLQMSRLRAEDSAVYFCFVKLGITY--FDSWGQGTLLTVS 118

QY 121 SASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPPTVSNWNGALTSGVHTFPAVLQS 180  
 DB 119 SASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPPTVSNWNGALTSGVHTFPAVLQS 178  
 QY 181 SGLYSLSWVTVFSSSLGTQTYICNVNHPKSNVTKVPEKSCDKTHPCPCPAPELLG 240  
 DB 179 SGLYSLSWVTVFSSSLGTQTYICNVNHPKSNVTKVPEKSCDKTHPCPCPAPELLG 238  
 QY 241 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREQY 300  
 DB 239 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREQY 298  
 QY 301 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 360  
 DB 299 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 358  
 QY 361 ELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 420  
 DB 359 ELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSR 418  
 QY 421 WQGNVFCSCVMHEALHNYTKQSLSPGK 451  
 DB 419 WQGNVFCSCVMHEALHNYTKQSLSPGK 449

RESULT 7  
 AAY29458  
 ID AAY29458 standard; Protein: 452 AA.  
 XX  
 AC AAY29458;  
 DT 05-OCT-1999 (first entry)  
 XX  
 DE Recombinant immunoglobulin SEQ ID NO:71.  
 XX  
 KW Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;  
 KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;  
 KW fusion protein.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9937779-A1.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 19-JAN-1999; 99WO-US01081.  
 XX  
 PR 24-JUL-1998; 98US-0122513.  
 PR 22-JAN-1998; 98US-0012116.  
 PR 20-FEB-1998; 98WO-US03337.  
 PR 24-JUL-1998; 98US-0121952.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;  
 PI Zapata GA;  
 XX  
 DR WPI; 1999-469134/39.  
 XX  
 PT New conjugates of nonproteinaceous polymers with antibody fragments,  
 PT used for treating inflammatory disorders  
 PS  
 PS Disclosure; Page 354-355; 360pp; English.  
 XX  
 CC The present invention describes a novel conjugate having one or more  
 CC antibody fragments covalently attached to one or more nonproteinaceous  
 CC polymer molecules, where the apparent size of the conjugate is at least  
 CC about 500 kDa. Conjugates of antibody fragments which bind the human  
 CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for  
 CC treating inflammatory disorders e.g. acute lung injury, ischemic  
 CC reperfusion disorder, and autoimmune diseases. They can also be used  
 CC for treating e.g. inflammatory skin diseases including psoriasis and



PD 15-FEB-2000.  
XX 20-FEB-1998; 98US-0027449.  
XX 21-FEB-1997; 97US-0038664.  
PR 22-JAN-1998; 98US-0074330.  
XX (GETH ) GENENTECH INC.  
XX Presta LG, Leong SR, Gonzalez TN;  
XX WPI; 2000-181809/16.  
XX New nucleic acid molecule encodes a polypeptide which is an  
PT anti-interleukin-8 monoclonal antibody or antibody fragment useful for  
PT the production of anti-interleukin-8 monoclonal antibodies or fragments  
PT -  
XX Examples; Columns 199-202; 188pp; English.  
XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody  
CC (MAB). The anti-IL-8 MAB comprises a sequence containing the CDRs  
CC (complementarity determining regions) of the humanized anti-IL-8  
CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized  
CC anti-IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments  
CC can be used in diagnosis, for affinity purification of IL-8 from  
CC recombinant cell culture or natural sources and for the treatment of  
CC inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic  
CC acids encoding the anti-IL-8 MAB can be associated in a vector with  
CC another gene encoding another protein or protein fragment to produce a  
CC fusion protein which can make isolation and/or purification of the  
CC protein an easier process.  
XX Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;  
Best Local Similarity 92.5%; Pred. No. 4e-124;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;  
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60  
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVWRQAPGKGLVWVSDPSNGETTY 60  
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCAK--HTGGGVMDPIDYWGQGLTVT 118  
Db 61 NQFKGRFTLSRDNSKNTLYIQMNSLRADTAIVYCARGYRNGDWF-FDVWGQGLTVT 119  
QY 119 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178  
Db 120 VSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179  
QY 179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAP 238  
Db 180 QSSGLYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAP 239  
QY 239 LGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298  
Db 240 LGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 299  
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
Db 300 QYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359  
QY 359 RDELTKNOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418  
Db 360 REMTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 419  
QY 419 SRQQGNVSCSVMEALHNHYTQKSLSLSPGK 451  
Db 420 SRQQGNVSCSVMEALHNHYTQKSLSLSPGK 452

RESULT 10

AAR42066  
ID AAR42066 standard; Protein; 459 AA.  
XX  
AC AAR42066;  
XX  
DT 29-APR-1994 (first entry)  
XX  
DE Human anti-HBs heavy chain.  
XX  
KW Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..9  
FT /label= sig\_peptide  
FT Protein 10..459  
FT /label= mat\_protein  
XX  
PN W09320205-A.  
XX  
PD 14-OCT-1993.  
XX  
PE 30-MAR-1993; 93WO-JP00396.  
XX  
PR 30-MAR-1992; 92JP-0074678.  
XX  
PA (SUNR ) SUNTORY LTD.  
XX  
PI Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
XX  
DR WPI; 1993-336913/42.  
DR N-PSDB; AA049944.  
XX  
XX Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PT  
XX Disclosure; Fig 6-8; 46pp; Japanese.  
XX  
CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in AAQ49943-Q49944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
XX  
SQ Sequence 459 AA;

Query Match 91.6%; Score 2207.5; DB 14; Length 459;  
Best Local Similarity 92.7%; Pred. No. 7e-124;  
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;  
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTYY 60  
Db 10 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVAVILYDGNHKEY 69  
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCAKHTGGGVMDPIDYWGQGLTVTVS 120  
Db 70 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCAKHTGGGVMDPIDYWGQGLTVTVS 128  
QY 121 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180  
Db 129 SASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 188  
QY 181 SGYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAP 240  
Db 189 SGYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAP 248  
QY 241 GPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQY 300  
Db 249 GPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQY 308  
QY 301 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSD 360  
Db 309 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSD 368





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XX WPI: 1994-007204/01.
DR N-PSDB; AAQ54655.
XX
XX New chimaeric T84.12 antibody active against carcinoembryonic
PT antigen - has murine variable and human constant regions, also
PT DNA encoding it and transformed myeloma cells
XX
XX Claim 1; Page 22-23; 27pp; English.
XX
XX The sequences (AAQ54651-52) show the light and heavy chain cDNAs
CC of murine T84.12. The T84.12 antibody is directed against the
CC tumour marker carcinoma embryonic antigen, and is useful for
CC tumour imaging and immunotherapy.
CC The amino acid sequence given in the specification has been
CC incorrectly identified as a nucleic acid sequence, therefore
CC unacceptable characters have been represented as an 'N'.
CC The amino acid sequence given below has been derived from the
CC cDNA, by the indexer.
XX
XX Sequence 477 AA;
SQ
Query Match 90.8%; Score 2190; DB 15; Length 477;
Best Local Similarity 91.08; Pred. No. 8e-123;
Matches 413; Conservative 16; Mismatches 17; Indels 8; Gaps 3;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
Db 29 EVKLVEGGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 87
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAHYCAK---HTGGGVDPIDYWGOGTLV 117
Db 88 VDSVKGRTISRDNKNTLYLQMSLRADTAHYCAKIDYGGG---FGYWGOGTLA 143
QY 118 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 177
Db 144 TVSAASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 203
QY 178 LQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKKVPPCKDTHTCPCPAPE 237
Db 204 LQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKKVPPCKDTHTCPCPAPE 263
QY 238 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKRE 297
Db 264 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKRE 323
QY 298 EQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPP 357
Db 324 EQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPP 383
QY 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 417
Db 384 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 443
QY 418 KSRWQCGNPFSCSVNHEALHNHYTQKSLSLSPGK 451
Db 444 KSRWQCGNPFSCSVNHEALHNHYTQKSLSLSPGK 477
RESULT 13
AAR24812
ID AAR24812 standard; Protein; 466 AA.
XX
XX AAR24812;
AC
XX
XX 28-DEC-1992 (first entry)
DT
XX
XX Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
DE
XX Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
XX antithrombotic agent; myocardial infarction therapy.
XX
XX Synthetic.
OS
```

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XX Key Location/Qualifiers
FH Peptide 13..19
FT /label= Leader
FT Region 20..134
FT /label= VH
FT Region 135..232
FT /label= CH1
FT Region 233..247
FT /label= hinge
FT Region 248..357
FT /label= CH2
FT Region 358..464
FT /label= CH3
FT Misc-difference 465
FT /note= "translated stop codon"
PN EP491351-A.
XX
XX 24-JUN-1992.
PD
XX
XX 17-DEC-1991; 91EP-0121591.
XX
XX 18-DEC-1990; 90JP-0413829.
PR
XX 11-NOV-1991; 91JP-0294464.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Iwasa S, Taka H, Watanabe T, Tada H;
XX
XX WPI: 1992-209528/26.
DR N-PSDB; AAQ25692.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
XX
XX Example; Figure 11; 87pp; English.
XX
XX plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prep'd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Aa-producing transformant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CLH
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'CLH and 3'C2H, of 5'EH and 3'CLH and of
CC 5'EH and 3'EH respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB.
XX
XX Sequence 466 AA;
SQ
Query Match 90.7%; Score 2186; DB 13; Length 466;
Best Local Similarity 90.9%; Pred. No. 1.4e-122;
Matches 410; Conservative 19; Mismatches 16; Indels 6; Gaps 2;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 60
Db 20 EVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGVWRQAPGKLEWVSGISGGSTYY 78
QY 61 ADSVKGRTISRDNKNTLYLQMSLRADTAHYCAKHTGGGVDPIDYWGOGTLVTVS 120
Db 79 PDSMKGRFTISRDNKNTLYLQMSLRADTAHYCAKHTGGGVDPIDYWGOGTLVTVS 133
QY 121 SASSTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 180
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Db 134 SASRKGVSFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 193
Qy 181 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPCPAPPELLG 240
Db 194 SGLYSLSVTVTPSSSLGTQTYICTVNHKPSNTKVDKVKPEKSCDKTHTCPCPAPPELLG 253
Qy 241 GPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQY 300
Db 254 GPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQY 313
Qy 301 NSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360
Db 314 NSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRE 373
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSR 420
Db 374 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSR 433
Qy 421 WQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 434 WQGNVFSCSVMHEALHNHYTQKSLSLSPGK 464

RESULT 14
AAR33311
ID AAR33311 standard; Protein; 453 AA.
XX
AC AAR33311;
XX
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaE11 Version 1 (intact IgG) heavy chain.
XX
KW Antibody; high affinity; FcEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; Fab; humael1v1.
XX
OS Synthetic.
XX
PN W09304173-A.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-0506860.
XX
PR 14-AUG-1991; 91US-0744768.
XX
PR 07-MAY-1992; 92US-0879495.
XX
PA (GETH ) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1993-094004/11.
XX
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and Vh
CC region kappa subgroup I). A first version, humael1v1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca.100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
XX
SQ Sequence 453 AA;
XX
Query Match 90.3%; Score 2177; DB 14; Length 453;
,Best Local Similarity 91.6%; Pred. No. 4.5e-122;

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Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
Qy 1 QYQLVQSGGLVQPGGSLRLSCAASGFTPRSN-AMGWVWPAQPKGLEWVSGTSGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYSTISGYSWHWIRQAPKGLWEVASIT-YDGSIN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTLLT 118
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTLLT 118
Qy 119 VSSAST--KGPSFPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPA 176
Db 119 VSSASTKKGSGSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPA 178
Qy 177 VLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPCPAP 236
Db 179 VLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKSCDKTHTCPCPAP 238
Qy 237 ELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPR 296
Db 239 ELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPR 298
Qy 297 EEQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLP 356
Db 299 EEQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLP 358
Qy 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLT 416
Db 359 PSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLT 418
Qy 417 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 419 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 15
AAY85199
ID AAY85199 standard; protein; 453 AA.
XX
AC AAY85199;
XX
DT 29-JUN-2000 (first entry)
XX
DE Heavy chain amino acid sequence of the humanised MaE11 antibody.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCBH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent; chimeric.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN US6037453-A.
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-0466151.
XX
PR 15-MAR-1995; 95US-0405617.
PR 14-AUG-1992; 92WO-US06860.
PR 26-JAN-1994; 94US-0185899.
XX
PA (GETH ) GENENTECH INC.
XX
PI Presta LG, Jardieu PM;
XX
DR WPI; 2000-269913/23.
XX
PT New bispecific antibodies, useful for treating immunoglobulin
PT E-mediated disease, binds to IgE, but only when on the low affinity
PT receptor, and to an antigen other than IgE -
XX
PS Claim 14; Fig 3; 48pp; English.

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XX This sequence represents the heavy chain amino acid sequence of a  
CC humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention  
CC relates to a bispecific antibody that binds specifically to IgE when IgE  
CC is bound to its low affinity receptor (FcεR), but does not bind to IgE,  
CC when IgE is bound to its high affinity receptor (FcεR). The bispecific  
CC antibody comprises an IgE-binding arm with human framework residues of a  
CC recipient human antibody and donor murine CDR (complementarity  
CC determining region) residues, but with at least one human CDR residue  
CC replacing the analogous murine residue. The antibody also comprises an Fv  
CC that is specific for a predetermined antigen other than IgE. The  
CC antibodies work by displacing bound IgE from its receptor, or via  
CC competitive inhibition of its binding. The bispecific antibodies are used  
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated  
CC diseases, also, when immobilised, for the isolation of FcεR from cells  
CC (for research or therapy). The bispecific antibodies of the invention do  
CC not cause granulation or release of histamine from mast cells.

XX SQ Sequence 453 AA;

Query Match 90.3%; Score 2177; DB 21; Length 453;  
Best Local Similarity 91.6%; Pred. No. 4.5e-122;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QYVLVSGGGLVQPGSLRLSCAASGFTFRSN-AMGWVROAPCKGLEWYSGISGGSGSTY 59  
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFRSN-AMGWVROAPCKGLEWYSGISGGSGSTY 59  
QY 60 YADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCAKHTG-GGYWDPIDYWGQGLTVT 118  
DB 60 YADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCAKHTG-GGYWDPIDYWGQGLTVT 118  
QY 119 VSSAST--KGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPA 176  
DB 119 VSSASTKGKPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPA 178  
QY 177 VLQSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAP 236  
DB 179 VLQSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCPAP 238  
QY 237 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296  
DB 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298  
QY 297 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 356  
DB 299 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 358  
QY 357 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTIV 416  
DB 359 PSREMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTIV 418  
QY 417 DKSRWQOGNWFSCVNHAEALHNHYTQKSLSLSPGK 451  
DB 419 DKSRWQOGNWFSCVNHAEALHNHYTQKSLSLSPGK 453

Search completed: October 9, 2002, 19:10:30  
Job time : 50.3214 secs



Db 61 NQKGRFTLSRDNKNTAYLQMSLRAEDTAVYYCARGDYRYNGDWF-FDVMGQGLT 119  
Qy 119 VSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEPVTVSWNSGALTSGVHTFP 178  
Db 120 VSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEPVTVSWNSGALTSGVHTFP 179  
Qy 179 QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVKFPCDKTHTCPCPAP 238  
Db 180 QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVKFPCDKTHTCPCPAP 239  
Qy 239 LGGSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYDGVVHNKTKPRE 298  
Db 240 LGGSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYDGVVHNKTKPRE 299  
Qy 299 QYNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358  
Db 300 QYNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 359  
Qy 359 RDELTKNOVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSGFFLYSL 418  
Db 360 REEMTKNOVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSGFFLYSL 419  
Qy 419 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451  
Db 420 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 452

## RESULT 4

US-08-157-101A-7  
; Sequence 7, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURLHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-157-101A-7

Query Match 91.6%; Score 2207.5; DB 1; Length 459;  
Best Local Similarity 92.7%; Pred. No. 1.5e-166;  
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;  
Qy 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGSGSTYY 60  
Db 10 QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVAVILYDGNHKEY 69  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYMGQGLTVTS 120  
Db 70 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYMGQGLTVTS 128  
Qy 121 SASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEPVTVSWNSGALTSGVHTFP 180  
Db 129 SASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEPVTVSWNSGALTSGVHTFP 188  
Qy 181 SGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVKFPCDKTHTCPCPAP 240  
Db 189 SGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVKFPCDKTHTCPCPAP 248  
Qy 241 GPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYDGVVHNKTKPRE 300  
Db 249 GPSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYDGVVHNKTKPRE 308  
Qy 301 NSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 360  
Db 309 NSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 368  
Qy 361 ELTKNOVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSGFFLYSL 420  
Db 369 ELTKNOVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSGFFLYSL 428  
Qy 421 WOQGNVFCSCVMHEALHNHYTKLSLSPGK 451  
Db 429 WOQGNVFCSCVMHEALHNHYTKLSLSPGK 459

## RESULT 5

US-08-466-151-8  
; Sequence 8, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992

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; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-8
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Query Match 90.3%; Score 2177; DB 3; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRSLCAASGFTRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRSLCAVSGYSITSGYSWNIHQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 296  
Db 239 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 298  
QY 297 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 6  
US-08-466-163B-8  
Sequence 8, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Presta, Paula M.  
APPLICANT: Jardieu, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14

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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-8
```

Query Match 90.3%; Score 2177; DB 3; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRSLCAASGFTRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRSLCAVSGYSITSGYSWNIHQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 296  
Db 239 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 298  
QY 297 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 6  
US-08-466-163B-8  
Sequence 8, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Presta, Paula M.  
APPLICANT: Jardieu, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14

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; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRP  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized maell, version 1 heavy chain  
US-08-466-163B-8
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Query Match 90.3%; Score 2177; DB 4; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVOLVQSGGGLVQPGGSLRLSAAAGFTFRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWNIRQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 296  
Db 239 ELGGGPSVFPLPCKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNAKT KPR 298  
QY 297 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 7  
US-08-887-352B-14  
Sequence 14, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Low  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.

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; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-8
```

Query Match 90.3%; Score 2177; DB 3; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRSLCAASGFTRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRSLCAVSGYSITSGYSWNIHQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 296  
Db 239 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 298  
QY 297 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 6  
US-08-466-163B-8  
Sequence 8, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Presta, Paula M.  
APPLICANT: Jardieu, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14

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; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 453 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-8
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Query Match 90.3%; Score 2177; DB 3; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRSLCAASGFTRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRSLCAVSGYSITSGYSWNIHQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 296  
Db 239 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 298  
QY 297 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 6  
US-08-466-163B-8  
Sequence 8, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Presta, Paula M.  
APPLICANT: Jardieu, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14

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; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 8  
; LENGTH: 453  
; TYPE: PRP  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized maell, version 1 heavy chain  
US-08-466-163B-8
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Query Match 90.3%; Score 2177; DB 4; Length 453;  
Best Local Similarity 91.6%; Pred. No. 3.8e-164;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVOLVQSGGGLVQPGGSLRLSAAAGFTFRSN--AMGWVRQAPGKGLEWVGISGGSTY 59  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNIHQAPGKLEWVASIT-YDGSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCAKHTG-GGVWDPIDYWGOGTLVT 118  
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRRAEDTAVYYCARSHYFGHHW-FAVMGOGTLVT 118  
QY 119 VSSAST--KGPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 176  
Db 119 VSSASTKRGKPSVFPLAPSSKTSGGTAALGCLVKIDYPPETPVTVSWNSGALTSGVHTPEA 178  
QY 177 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 236  
Db 179 VLQSSGLYSLSSVTVTPSSSLGTQTICNVNHKPKNTKDKKVEPKSCDKTHCCPCPAP 238  
QY 237 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 296  
Db 239 ELGGGPSVFPLPSPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNNAKT KPR 298  
QY 297 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 356  
Db 299 EEOYNSTIRYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLP 358  
QY 357 PSRDDELTKNOVSITCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 416  
Db 359 PSREEMTKNQVSLTCLVKGYFSDIAEVESNGQPENNYKTTPTPPVLDSDGSFFLYSK LTV 418  
QY 417 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451  
Db 419 DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453

RESULT 7  
US-08-887-352B-14  
Sequence 14, Application US/08887352B  
Patent No. 5994511  
GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Low  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
TITLE OF INVENTION: Improving Polypeptides  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,352B  
FILING DATE: 03-Jul-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.

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;
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-14

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Query Match          90.0%; Score 2169; DB 2; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

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QY 1 QVOLVSGGGLVOPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGISGGSTY 59
Db 1 EVQLVESGGGLVOPGGSLRLSCAVSYISITGYSWNWIRQAPGKLEWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLTV 118
Db 60 YNPVKGRITISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGLTV 118
QY 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 239 LGGPSVFLPPPKPKDILMSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
Db 239 LGGPSVFLPPPKPKDILMSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
QY 299 QYNSTRYRVSVLVTHQDWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTRYRVSVLVTHQDWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

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RESULT 8
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997

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;
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-16

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Query Match          90.0%; Score 2169; DB 2; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

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QY 1 QVOLVSGGGLVOPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGISGGSTY 59
Db 1 EVQLVESGGGLVOPGGSLRLSCAVSYISITGYSWNWIRQAPGKLEWVASIT-YDGSIN 59
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLTV 118
Db 60 YNPVKGRITISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGLTV 118
QY 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVL 178
QY 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Db 179 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 239 LGGPSVFLPPPKPKDILMSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
Db 239 LGGPSVFLPPPKPKDILMSRTEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
QY 299 QYNSTRYRVSVLVTHQDWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 299 QYNSTRYRVSVLVTHQDWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

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RESULT 9
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET INFORMATION: P0718P2CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 90.0%; Score 2169; DB 3; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASIT-YDGSN 59
60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICAKHTG-GGYWDPIDYWGQGLTV 118
60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHWH-FAVWGQGLTV 118
119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
239 LGGPSVFLFPPPKDPTLMISRTPETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
239 LGGPSVFLFPPPKDPTLMISRTPETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
359 RDELTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
359 REEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
419 SRWQOGNVFSCSVMHREALNHYTQKSLSPGK 451
419 SRWQOGNVFSCSVMHREALNHYTQKSLSPGK 451

RESULT 10
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
;
GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE OF INVENTION: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial

; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASIT-YDGSN 59
60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICAKHTG-GGYWDPIDYWGQGLTV 118
60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYICARGSHYFGHWH-FAVWGQGLTV 118
119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVL 178
179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
239 LGGPSVFLFPPPKDPTLMISRTPETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
239 LGGPSVFLFPPPKDPTLMISRTPETCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298
299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
359 RDELTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
359 REEMTKNOVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
419 SRWQOGNVFSCSVMHREALNHYTQKSLSPGK 451
419 SRWQOGNVFSCSVMHREALNHYTQKSLSPGK 451

RESULT 11
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
;
GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE OF INVENTION: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial



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; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-109-207C-16

Query Match          90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGVWRQAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASIT-YDGSTN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVMGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178

QY 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451

RESULT 12
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-14

Query Match          90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGVWRQAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASIT-YDGSTN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVMGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178

QY 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451

RESULT 13
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypepti
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-16

Query Match          90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGVWRQAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWVASIT-YDGSTN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVMGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL 178

QY 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 OSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGSPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 299 QYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451

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Db 359 REEMTKNOYSLTCLYKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

Qy 419 SRWQGNVFSQSYMHEALHNHYTQKSLSLSPGK 451

Db 419 SRWQGNVFSQSYMHEALHNHYTQKSLSLSPGK 451

Search completed: October 9, 2002, 19:14:06  
Job time : 20.4082 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:10:35 ; Search time 177.754 seconds  
(without alignments)  
893.051 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALHNYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*  
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24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.\*  
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26: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2411	100.0	451	22	US-09-822-698A-26
2	2228.5	92.4	475	7	US-08-309-530-4
3	2228.5	92.4	663	1	PCT-US01-32140-32
4	2228.5	92.4	4852	1	PCT-US01-32140-33
5	2224.5	92.3	499	21	US-09-760-479-645
6	2223.5	92.2	494	21	US-09-760-479-636
7	2214.5	91.8	449	20	US-09-680-148-2

8	2212	91.7	464	21	US-09-751-181-26	Sequence 26, Appl
9	2211.5	91.7	452	14	US-09-012-116-71	Sequence 71, Appl
10	2211.5	91.7	452	15	US-09-121-952A-71	Sequence 71, Appl
11	2211.5	91.7	452	15	US-09-122-513A-71	Sequence 71, Appl
12	2211.5	91.7	452	16	US-09-234-182A-71	Sequence 71, Appl
13	2211.5	91.7	452	16	US-09-234-340A-71	Sequence 71, Appl
14	2211.5	91.7	452	18	US-09-489-394-71	Sequence 71, Appl
15	2211.5	91.7	452	21	US-09-726-258-71	Sequence 71, Appl
16	2207.5	91.6	459	5	US-08-157-101-7	Sequence 7, Appl
17	2196	91.1	476	21	US-09-760-479-599	Sequence 599, App
18	2177	90.3	453	7	US-08-328-597-8	Sequence 8, Appl
19	2177	90.3	453	8	US-08-405-617-8	Sequence 8, Appl
20	2177	90.3	453	22	US-09-802-077-8	Sequence 8, Appl
21	2177	90.3	453	22	US-09-802-096-8	Sequence 8, Appl
22	2177	90.3	453	23	US-09-925-179-8	Sequence 8, Appl
23	2169	90.0	451	12	US-08-887-352-14	Sequence 14, Appl
24	2169	90.0	451	12	US-08-887-352-16	Sequence 16, Appl
25	2169	90.0	451	12	US-08-887-352A-14	Sequence 14, Appl
26	2169	90.0	451	12	US-08-887-352A-16	Sequence 16, Appl
27	2169	90.0	451	15	US-09-109-207-14	Sequence 14, Appl
28	2169	90.0	451	15	US-09-109-207-16	Sequence 16, Appl
29	2169	90.0	451	15	US-09-109-207-14	Sequence 14, Appl
30	2169	90.0	451	15	US-09-109-207-16	Sequence 16, Appl
31	2169	90.0	451	21	US-09-716-028-14	Sequence 14, Appl
32	2169	90.0	451	21	US-09-716-028-16	Sequence 16, Appl
33	2169	90.0	451	23	US-09-920-171-14	Sequence 14, Appl
34	2169	90.0	451	23	US-09-920-171-16	Sequence 16, Appl
35	2169	90.0	451	23	US-09-925-179-65	Sequence 65, Appl
36	2168	89.9	451	12	US-08-887-352-18	Sequence 18, Appl
37	2168	89.9	451	12	US-08-887-352A-18	Sequence 18, Appl
38	2168	89.9	451	15	US-09-109-207-18	Sequence 18, Appl
39	2168	89.9	451	15	US-09-109-207-18	Sequence 18, Appl
40	2168	89.9	451	16	US-09-282-846-2	Sequence 2, Appl
41	2168	89.9	451	18	US-09-483-588-2	Sequence 2, Appl
42	2168	89.9	451	20	US-09-680-145-2	Sequence 2, Appl
43	2168	89.9	451	21	US-09-713-425-2	Sequence 2, Appl
44	2168	89.9	451	21	US-09-716-028-18	Sequence 18, Appl
45	2168	89.9	451	21	US-09-792-938-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; TYPE: PRT  
; LENGTH: 451  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1  
US-09-822-698A-26

Query Match 100.0%; Score 2411; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-186;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLVQSGGGLVQPGGSLRLCAASGGFTFRSNAMGWVRQAPGKLEWVSGISGGSGTYY 60  
DB 1 QVQLVQSGGGLVQPGGSLRLCAASGGFTFRSNAMGWVRQAPGKLEWVSGISGGSGTYY 60

Qy	61	ADSVKGRFTISRDNSKNTLYIQNNSIARAEDTAIVYCAKHTGGVWDPIDTWGGOTLVTVS	120
Db	61	ADSVKGRFTISRDNSKNTLYIQNNSIARAEDTAIVYCAKHTGGVWDPIDTWGGOTLVTVS	120
Qy	121	SASVTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS	180
Db	121	SASVTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS	180
Qy	181	SLGLYSLSVTVTPSSSLGTQTYICNVNHPKSTKVYDKKVEPKSCDKHTCCPCPAPPELLG	240
Db	181	SLGLYSLSVTVTPSSSLGTQTYICNVNHPKSTKVYDKKVEPKSCDKHTCCPCPAPPELLG	240
Qy	241	GPSVFLFPKPKDPLMTISRPEVTVCVVDVDSHEDPEVFENNYVDGVEVHNAKTKPREEQY	300
Db	241	GPSVFLFPKPKDPLMTISRPEVTVCVVDVDSHEDPEVFENNYVDGVEVHNAKTKPREEQY	300
Qy	301	NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRD	360
Db	301	NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKTISKAKGQPREPQVYTLPPSRD	360
Qy	361	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGFFLYSKLTVDKSR	420
Db	361	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGFFLYSKLTVDKSR	420
Qy	421	WQGGVVFSCSYMHEALHNHYTKQSLSLSPGK	451
Db	421	WQGGVVFSCSYMHEALHNHYTKQSLSLSPGK	451

## RESULT 2

RESOLUTION 2  
US-08-309-530-4  
; Sequence 4, Application US/08309530  
; GENERAL INFORMATION:  
; APPLICANT: FELGENHAUER, MARTIN; HIMMLER, GOTTFRIED; KOHN,  
; APPLICANT: JOHANN; AND STEINDL, FRANZ  
; TITLE OF INVENTION: RECOMBINANT PROTEIN WHICH  
; TITLE OF INVENTION: BINDS TO A COMPLEX VIRAL ANTIGEN OF HIV-1

[illegible]

РЕСПУБЛИКА

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RESULT 3
PCT-US01-32140-32
; Sequence 32, Application PC/TUS0132140
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: A100 PCT
; CURRENT APPLICATION NUMBER: PCT/US01/32140
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT

```

; ORGANISM: Homo Sapien	
PCT-US01-32140-32	
Query Match 92.4%; Score 2228.5; DB 1; Length 663;	
Best Local Similarity 93.3%; Pred. No. 1.5e-171;	
Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;	
QY 1	QVQLVQSGGGLVQPGGSLRLS
DB 215	EVQLVESGGGLVQPGGSLRLS
QY 61	ADSVKGRFTISRDNKNTLYIQMNSLRAEDTAVYICAKHTGGGVNDPIDYWGQGLTVTVS
DB 275	PDVSKGRFTISRDNKNTLYIQMNSLRAEDTAVYICAREENGNYFY-YFDYWGQGLTVTVS
QY 121	SASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
DB 334	SASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
QY 181	SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELIG
DB 394	SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELIG
QY 241	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQY
DB 454	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREQY
QY 301	NSTYRVSVSLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRD
DB 514	NSTYRVSVSLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRD
QY 361	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
DB 574	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
QY 421	WQGNVFCFSVMHEALHNHYTKQSLSPG 450
DB 634	WQGNVFCFSVMHEALHNHYTKQSLSPG 663
RESULT 4	
PCT-US01-32140-33	
; Sequence 33, Application PC/TUS0132140	
; GENERAL INFORMATION:	
; APPLICANT: BIOGEN, INC.	
; APPLICANT: GABER, Ellen	
; APPLICANT: LYNE, Paul	
; APPLICANT: SALDHANA, Jose W.	
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES	
; FILE REFERENCE: A100 PCT	
; CURRENT APPLICATION NUMBER: PCT/US01/32140	
; CURRENT FILING DATE: 2001-10-12	
; PRIOR APPLICATION NUMBER: 60/240,285	
; PRIOR FILING DATE: 2000-10-13	
; PRIOR APPLICATION NUMBER: 60/275,289	
; PRIOR FILING DATE: 2001-03-13	
; PRIOR APPLICATION NUMBER: 60/299,987	
; PRIOR FILING DATE: 2001-06-21	
; NUMBER OF SEQ ID NOS: 33	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 33	
; LENGTH: 4852	
; TYPE: PRT	
; ORGANISM: Homo Sapien	
PCT-US01-32140-33	
Query Match 92.4%; Score 2228.5; DB 1; Length 4852;	
Best Local Similarity 93.3%; Pred. No. 2.4e-170;	
Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;	
QY 1	QVQLVQSGGGLVQPGGSLRLS
DB 4404	EVQLVESGGGLVQPGGSLRLS
; ORGANISM: Homo Sapien	
PCT-US01-32140-33	
Query Match 92.3%; Score 2224.5; DB 21; Length 499;	
Best Local Similarity 91.9%; Pred. No. 2.1e-171;	
Matches 421; Conservative 13; Mismatches 17; Indels 7; Gaps 2;	
QY 1	QVQLVQSGGGLVQPGGSLRLS
DB 42	QVQLVQSGGGLVQPGGSLRLS
QY 61	ADSVKGRFTISRDNKNTLYIQMNSLRAEDTAVYICAKHTGGGVNDPIDYWGQGLTVTVS
DB 102	GDSVGRFTISRDNKNTLYIQMNSLRAEDTAVYICAREENGNYFY-YFDYWGQGLTVTVS
QY 114	GLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHT
DB 162	GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHT
QY 174	FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPC
DB 222	FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPC
QY 234	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATK
DB 282	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATK
QY 294	KPREQYNSTYRVSVSLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVY

Db 342 KPREQYNSTRVSVLTVLHODWLNCKEYCKVSNKALPAPIEKTISKAKGPREQVY 401  
QY 354 TLPPSRDELTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSK 413  
Db 402 TLPPSRDELTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSK 461  
QY 414 LTVDKSRQOQNVFSCSVMHREALHNYTKSLSPGK 451  
Db 462 LTVDKSRQOQNVFSCSVMHREALHNYTKSLSPGK 499

RESULT 6

US-09-760-479-636  
; Sequence 636, Application US/09760479  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT#53  
; CURRENT APPLICATION NUMBER: US/09/760,479  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 946  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 636  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-479-636

Query Match 92.2%; Score 2223.5; DB 21; Length 494;  
Best Local Similarity 93.0%; Pred. No. 2.5e-171;  
Matches 422; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGSGSYIY 60  
Db 41 EVQLVESGGGLVQPGGSLRLSCAAAEAFSNYMHVWRQAPGKGLLWVSHLNSDGSSTRY 100  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK--HTGGGVNDP-IDYWGQGLTV 117  
Db 101 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARGVKTGSSWSPDFDYWGQGLTV 160  
QY 118 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 177  
Db 161 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 220  
QY 178 LQSSGLYSLSSVYTPVSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPE 237  
Db 221 LQSSGLYSLSSVYTPVSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPE 280  
QY 238 LLGGPSVFLPPKPKDITLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPRE 297  
Db 281 LLGGPSVFLPPKPKDITLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPRE 340  
QY 298 EQYNSTRYVSVLTVLHODWLNCKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 357  
Db 341 EQYNSTRYVSVLTVLHODWLNCKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 400  
QY 358 SRDELTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTV 417  
Db 401 SRDELTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTV 460  
QY 418 KSRWQOQNVFSCSVMHREALHNYTKSLSPGK 451  
Db 461 KSRWQOQNVFSCSVMHREALHNYTKSLSPGK 494

RESULT 7

US-09-680-148-2  
; Sequence 2, Application US/09680148  
; GENERAL INFORMATION:  
; APPLICANT: BASEY, CAROL D.  
; APPLICANT: BLANK, GREG S.

; TITLE OF INVENTION: PROTEIN PURIFICATION  
; FILE REFERENCE: P1241R1D1  
; CURRENT APPLICATION NUMBER: US/09/680,148  
; CURRENT FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: US 60/084,459  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: US 09/304,465  
; PRIOR FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
US-09-680-148-2

Query Match 91.8%; Score 2214.5; DB 20; Length 449;  
Best Local Similarity 92.7%; Pred. No. 1.2e-170;  
Matches 417; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGSGSYIY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVARIYPTNGYTRY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGGVNDPIDYWGQGLTVTVS 120  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCSRWGGDGFY-AMDYWGQGLTVTVS 119  
QY 121 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLOS 180  
Db 120 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLOS 179  
QY 181 SGYLSLSSVYTPVSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPELLG 240  
Db 180 SGYLSLSSVYTPVSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPELLG 239  
QY 241 GPSVFLPPKPKDITLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300  
Db 240 GPSVFLPPKPKDITLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 299  
QY 301 NSTYRVVSVLTVLHODWLNCKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 360  
Db 300 NSTYRVVSVLTVLHODWLNCKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 359  
QY 361 ELTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSR 420  
Db 360 EMTKNOVSLCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSR 419  
QY 421 WQOQNVFSCSVMHREALHNYTKSLSPG 450  
Db 420 WQOQNVFSCSVMHREALHNYTKSLSPG 449

RESULT 8

US-09-751-181-26  
; Sequence 26, Application US/09751181  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp  
; TITLE OF INVENTION: Specific Human Antibodies for Selective Cancer Therapy  
; FILE REFERENCE: 456  
; CURRENT APPLICATION NUMBER: US/09/751,181  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 202  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-751-181-26

Query Match 91.7%; Score 2212; DB 21; Length 464;  
Best Local Similarity 92.9%; Pred. No. 2e-170;



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Matches 418; Conservative 13; Mismatches 13; Indels 6; Gaps 2;
QY 2 VOLVQSGGLVOPGGSLRLSCAASGFTFERSNAMGWVRAQPKGLEWVSGTSGSGSTYYA 61
Db 21 IQLVESGGGVVPRPGGSLRLSCAASGFTFDDYGMKSWVRAQPKGLEWVSGINWNGGSTGYA 80
QY 62 DSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVSS 121
Db 81 DSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVSS 134
QY 122 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 181
Db 135 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 194
QY 182 GLYSLSVTVVPSLSGLTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPAPPELLGG 241
Db 195 GLYSLSVTVVPSLSGLTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPAPPELLGG 254
QY 242 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNHYVDGVEVHNATKPREQYN 301
Db 255 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNHYVDGVEVHNATKPREQYN 314
QY 302 STRVSVSLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 361
Db 315 STRVSVSLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 374
QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 421
Db 375 MTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 434
QY 422 QCNQVFSCSVMHREALNHYTKQSLSLSPGK 451
Db 435 QCNQVFSCSVMHREALNHYTKQSLSLSPGK 464

RESULT 9
US-09-012-116-71
; Sequence 71, Application US/09012116
; GENERAL INFORMATION:
; APPLICANT: Hsei, Vanessa
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo
; APPLICANT: Koumenis, Iphigenia
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,116
; FILING DATE: 22-Jan-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-012-116-71
Query Match 91.7%; Score 2211.5; DB 14; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
QY 1 QVOLVQSGGLVOPGGSLRLSCAASGFTFERSNAMGWVRAQPKGLEWVSGTSGSGSTYYA 60
Db 1 EQVLVQSGGLVOPGGSLRLSCAASGYSFSSHYHWHVRAQPKGLEWVGYIDPSNGETTY 60
QY 61 ADSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCAK--HTGGVWDPIIDYWGQGLTVT 118
Db 61 NOKFKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCARGDYRYNGDMF-FDWMGQGLTVT 119
QY 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVL 178
Db 120 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVL 179
QY 179 QSGGLYSLSVTVVPSLSGLTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPAPPELL 238
Db 180 QSGGLYSLSVTVVPSLSGLTQTYICNVNHPKSNKYDKKVEPKSCDKTHTCPPAPPELL 239
QY 239 LGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNHYVDGVEVHNATKPREE 298
Db 240 LGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNHYVDGVEVHNATKPREE 299
QY 299 QYNSTVRVSVSLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 300 QYNSTVRVSVSLTVLHQDLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALNHYTKQSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALNHYTKQSLSLSPGK 452

RESULT 10
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
```

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; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-121-952A-71

Query Match          91.7%; Score 2211.5; DB 15; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLQSGGLVQPGSLRLSCAASGFTFRSNAWGVRQAPGKGLWVGISGSGSTYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFSSHYHWHVRQAPGKGLWVGIDPSNGEITY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTVT 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDMF-FDVMGQGLTVT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGLVLDYFPEPVTYVSNWSGALTSVHTFPFPAVL 178
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGLVLDYFPEPVTYVSNWSGALTSVHTFPFPAVL 179

QY 179 QSSGLYLSLVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 QSSGLYLSLVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 239

QY 239 LGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 LGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299

QY 299 QYASTYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 QYNSTYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359

QY 359 RDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 418
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 REEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 419

QY 419 SRWQOGNVFSCVMHEALHNHYTOKLSLSLSPGK 451
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 SRWQOGNVFSCVMHEALHNHYTOKLSLSLSPGK 452

RESULT 11
US-09-122-513A-71
; Sequence 71, Application US/09122513A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shatrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
```

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; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,513A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-122-513A-71

Query Match          91.7%; Score 2211.5; DB 15; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLQSGGGLVQPGSLRLSCAASGFTFRSNAWGVRQAPGKGLWVGISGSGSTYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGGLVQPGSLRLSCAASGYFSFSSHYHWHVRQAPGKGLWVGIDPSNGEITY 60

QY 61 ADSVKGRTTISRDNKNTLYLQMNLSRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTVT 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDMF-FDVMGQGLTVT 119

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGLVLDYFPEPVTYVSNWSGALTSVHTFPFPAVL 178
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGLVLDYFPEPVTYVSNWSGALTSVHTFPFPAVL 179

QY 179 QSSGLYLSLVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 QSSGLYLSLVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 239

QY 239 LGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 LGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299

QY 299 QYNSTYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 QYNSTYRVVSVLTVLDHQLNGKEVKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359

QY 359 RDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 418
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 REEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 419

QY 419 SRWQOGNVFSCVMHEALHNHYTOKLSLSLSPGK 451
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 SRWQOGNVFSCVMHEALHNHYTOKLSLSLSPGK 452

RESULT 12
US-09-234-182A-71
; Sequence 71, Application US/09234182A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
```

APPLICANT: Koumenis, Iphigenia  
 APPLICANT: Leong, Steven R.  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Shahrokh, Zahra  
 APPLICANT: Zapata, Gerardo A.  
 TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
 NUMBER OF SEQUENCES: 72  
 TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/234,182A

FILING DATE: 20-Jan-1999

CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/074330

FILING DATE: 22-JAN-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/094003

FILING DATE: 24-JUL-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/094013

FILING DATE: 24-JUL-1998

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/075467

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4-1A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 452 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-234-182A-71

Query Match 91.7%; Score 2211.5; DB 16; Length 452;

Best Local Similarity 92.5%; Pred. No. 2.le-170;

Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGSGSTYY 60

DB 1 EVOLVQSGGLVQPGGSLRLSCAASGYSFSSHYMHVWROAPGKGLWVGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADDTAVYCAK--HTGGGVWDPIDYWGQGLTVT 118

DB 61 NQKFKGRFTLSRDNSKNTLYIQMNSLRADDTAVYCAARGDYRYNGDWF-FDYWGQGLTVT 119

QY 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 179 QSSGLYSLSVTVVPSVSSSLGCTQYICNVNHPKSTYVDKVEPKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSVTVVPSVSSSLGCTQYICNVNHPKSTYVDKVEPKSCDKTHTCPPCPAPEL 239

QY 239 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNRYVDGVVHRAKTKPREE 298

DB 240 LGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNRYVDGVVHRAKTKPREE 299

QY 299 QYNSTYRVSVLTIVLHODWLNKKEYCKYSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
 DB 300 QYNSTYRVSVLTIVLHODWLNKKEYCKYSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359  
 QY 359 RDELTKNOVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSEFLYSKLTVDK 418  
 DB 360 REEMTKNOVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSEFLYSKLTVDK 419  
 QY 419 SRWQOGNVFSCVMHEALHNHYTKLSLSLSPGK 451  
 DB 420 SRWQOGNVFSCVMHEALHNHYTKLSLSLSPGK 452

RESULT 13

US-09-234-340A-71

; Sequence 71, Application US/09234340A

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Haei, Vanessa

; APPLICANT: Koumenis, Iphigenia

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Shahrokh, Zahra

; APPLICANT: Zapata, Gerardo A.

; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/234,340A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/121,952

; FILING DATE: 24-Jul-1998

; APPLICATION NUMBER: 60/074330

; FILING DATE: 22-JAN-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/075467

; FILING DATE: 20-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1085R4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; US-09-234-340A-71

Query Match 91.7%; Score 2211.5; DB 16; Length 452;

Best Local Similarity 92.5%; Pred. No. 2.le-170;

Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGSGSTYY 60

DB 1 EVOLVQSGGLVQPGGSLRLSCAASGYSFSSHYMHVWROAPGKGLWVGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRONSKNTLYLQNSLRADTAVYCAK--HTGGGVWDPIDWGQGLT 118  
Db 61 NQKFKGRTISRONSKNTAYLQNSLRADTAVYCAKRGDYNDWPF-FDVGQGLT 119  
QY 119 VSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWSGALTSVHTFFAVL 178  
Db 120 VSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWSGALTSVHTFFAVL 179  
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPCPAPEL 238  
Db 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPCPAPEL 239  
QY 239 LGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREE 298  
Db 240 LGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREE 299  
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 358  
Db 300 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 359  
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDK 418  
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDK 419  
QY 419 SRWQGNVFCVSNVHHEALHNHYTQKSLSLSPGK 451  
Db 420 SRWQGNVFCVSNVHHEALHNHYTQKSLSLSPGK 452

RESULT 14  
US-09-489-394-71  
; Sequence 71, Application US/09489394  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND USES OF SAME  
; FILE REFERENCE: P1085R6  
; CURRENT APPLICATION NUMBER: US/09/489,394  
; EARLIER FILING DATE: 2000-01-21  
; EARLIER APPLICATION NUMBER: US 60/116,787  
; EARLIER FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 71  
; LENGTH: 452  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-452  
; OTHER INFORMATION: recombinant immunoglobulin  
US-09-489-394-71

Query Match 91.7%; Score 2211.5; DB 18; Length 452;  
Best Local Similarity 92.5%; Pred. No. 2.1e-170;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLGLEWVSGISGGSGSTYY 60  
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHHMHWVROAPGKLGLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRONSKNTLYLQNSLRADTAVYCAK--HTGGGVWDPIDWGQGLT 118  
Db 61 NQKFKGRTISRONSKNTAYLQNSLRADTAVYCAKRGDYNDWPF-FDVGQGLT 119  
QY 119 VSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWSGALTSVHTFFAVL 178  
Db 120 VSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWSGALTSVHTFFAVL 179  
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPCPAPEL 238  
Db 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPCPAPEL 239

Db 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSCDKTHTCPCPAPEL 239  
QY 239 LGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREE 298  
Db 240 LGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNKTKPREE 299  
QY 299 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 358  
Db 300 QYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 359  
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDK 418  
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDK 419  
QY 419 SRWQGNVFCVSNVHHEALHNHYTQKSLSLSPGK 451  
Db 420 SRWQGNVFCVSNVHHEALHNHYTQKSLSLSPGK 452

RESULT 15  
US-09-726-258-71  
; Sequence 71, Application US/09726258  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/726,258  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/234,182  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/094003  
; FILING DATE: 24-JUL-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 452 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-726-258-71

Query Match 91.7%; Score 2211.5; DB 21; Length 452;  
Best Local Similarity 92.5%; Pred. No. 2.1e-170;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLGLEWVSGISGGSGSTYY 60

Db	1	EVOLVQSGGLVQVGGSLRLSCAAGSYSSSHYMHWRQAPCKGLEWVGYIDPSNGETTY	60
QY	61	ADSVKGRFTISRDNSKNTLYIQWNSLRAREDYAVYCAK--HTGGGVNDPTDYNGQGTFLT	118
Db	61	NOKFKGRFTLIRDNSKNTAYIQWNSLRAREDYAVYCAAGDYRYNGDMF-FDWMQGTFLT	119
QY	119	VSSASTKPSVFPLAPSSKSTSGTAAALGCLVKDYFPPETVSVNSGALTSGVHTEPAVL	178
Db	120	VSSASTKPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTEPAVL	179
QY	179	QSSGLYSLSVVYTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTCTCPCPAPEL	238
Db	180	QSSGLYSLSVVYTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKTCTCPCPAPEL	239
QY	239	LGSPSVFLFPKPKDITLMI SRTPEVTCVVVDYSHEDPEPKFNWYDGVGVHNAKTKPRE	298
Db	240	LGSPSVFLFPKPKDITLMI SRTPEVTCVVVDYSHEDPEKFNWYDGVGVHNAKTKPRE	299
QY	299	QYNSTYRYVSVTLVHQQWLNQGEYKCKVSNKALPAPIEKTISKAKGPREPVYTLPPS	358
Db	300	QYNSTYRYVSVTLVHQQWLNQGEYKCKVSNKALPAPIEKTISKAKGPREPVYTLPPS	359
QY	359	REELTKNOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTPTPLVDSGSFFLSKLTVDK	418
Db	360	REELTKNOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTPTPLVDSGSFFLSKLTVDK	419
QY	419	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	451
Db	420	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	452

Search completed: October 9, 2002, 19:19:31  
Job time : 181.754 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 : Search time 59,8265 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALNHYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US05\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	2270	94.2	449	5	US-09-736-371-21	Sequence 21, Appl
2	2270	94.2	449	5	US-09-736-371B-21	Sequence 21, Appl
3	2245	93.1	449	1	PCT-US02-11853-12	Sequence 12, Appl
4	2245	93.1	468	1	PCT-US02-11853-20	Sequence 20, Appl
5	2236.5	92.8	442	1	PCT-US02-21323-12	Sequence 12, Appl
6	2236.5	92.8	442	1	PCT-US02-21324-12	Sequence 12, Appl
7	2236.5	92.8	442	1	PCT-US02-26321-12	Sequence 12, Appl
8	2229.5	92.5	477	5	US-09-791-537-118979	Sequence 118979,
9	2226.5	92.3	442	1	PCT-US02-21323-21	Sequence 21, Appl
10	2226.5	92.3	442	1	PCT-US02-21324-21	Sequence 21, Appl
11	2226.5	92.3	442	1	PCT-US02-26321-16	Sequence 16, Appl
12	2224.5	92.3	499	6	US-10-206-008-645	Sequence 645, App
13	2223.5	92.2	494	6	US-10-206-008-636	Sequence 636, App
14	2216	91.9	582	6	US-10-089-500-53	Sequence 53, Appl
15	2214.5	91.8	449	5	US-09-304-465A-2	Sequence 2, Appli
16	2214.5	91.8	449	5	US-10-253-366-2	Sequence 2, Appli
17	2209.5	91.6	473	5	US-09-791-537-118977	Sequence 118977
18	2196	91.1	476	6	US-10-206-008-599	Sequence 599, App
19	2189	90.8	470	6	US-10-020-047-3730	Sequence 3730, Ap
20	2181	90.5	470	6	US-10-020-786-9	Sequence 9, Appli
21	2172.5	90.1	444	5	US-09-674-716B-53	Sequence 53, Appl
22	2171	90.0	582	6	US-10-089-500-57	Sequence 57, Appl
23	2170	90.0	476	6	US-10-020-786-11	Sequence 11, Appl
24	2169	90.0	451	6	US-10-113-996-14	Sequence 14, Appl
25	2169	90.0	451	6	US-10-113-996-16	Sequence 16, Appl
26	2169	90.0	451	6	US-10-019-586-2	Sequence 2, Appli

27	2168	89.9	451	6	US-10-113-996-18	Sequence 18, Appl
28	2162.5	89.7	467	5	US-09-791-537-132460	Sequence 132460,
29	2160	89.6	478	5	US-09-758-173-8	Sequence 8, Appli
30	2160	89.6	478	5	US-09-526-098-8	Sequence 8, Appli
31	2160	89.6	478	5	US-09-948-429B-8	Sequence 8, Appli
32	2160	89.6	478	5	US-09-971-631-8	Sequence 8, Appli
33	2160	89.6	478	6	US-10-124-807-8	Sequence 8, Appli
34	2160	89.6	478	6	US-10-124-905-8	Sequence 8, Appli
35	2160	89.6	478	6	US-10-030-390-8	Sequence 8, Appli
36	2158.5	89.5	455	5	US-09-791-537-95084	Sequence 95084, A
37	2135.5	88.6	467	1	PCT-US02-20181-2	Sequence 2, Appli
38	2131	88.4	478	6	US-10-104-047-3812	Sequence 3812, Ap
39	2115	87.7	430	6	US-10-206-008-715	Sequence 715, App
40	2115	87.7	430	6	US-10-211-364-1052	Sequence 1052, Ap
41	2113.5	87.7	469	5	US-09-791-537-32261	Sequence 32261, A
42	2109.5	87.5	465	6	US-10-031-355-5	Sequence 5, Appli
43	2109.5	87.5	465	6	US-10-031-355-12	Sequence 12, Appl
44	2106.5	87.4	448	1	PCT-US01-27352-2	Sequence 2, Appli
45	2102.5	87.2	489	6	US-10-104-047-3329	Sequence 3329, Ap

ALIGNMENTS

RESULT 1

US-09-736-371-21  
; Sequence 21, Application US/09736371  
; GENERAL INFORMATION:

; APPLICANT: Waldmann, Herman  
; APPLICANT: Frewin, Mark  
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES  
; FILE REFERENCE: Waldmann  
; CURRENT APPLICATION NUMBER: US/09/736,371  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: 9815909.8  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: PCT/GB99/02380  
; PRIOR FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-736-371-21

Query Match	Best Local Similarity	94.2%;	Score 2270;	DB 5;	Length 449;
Matches 431;	Conservative	5;	Mismatches 10;	Indels	8; Gaps
QY	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKGLVWVSGISGGSTYY	60		
Db	1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSFPMWVQAPGKGLVWVSTISGGRTYY	60		
QY	61	ADSVKGRFTISRDNSKNTLYLQMNSLRADETAVYYCAK---HTGGGVWDPIDYWGQGLTV	117		
Db	61	RDVSKGRFTISRDNSKNTLYLQMNSLRADETAVYYCAKFRQYSGG-----FDWGGQGLTV	115		
QY	118	TVSSASTKGPSVFPIPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV	177		
Db	116	TVSSASTKGPSVFPIPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV	175		
QY	178	LOSSGGLYSLSVVTVVSSSLGQTIVICNVNHPKSNVTKVDKVEPKSCDKHTHTCPCPAPE	237		
Db	176	LQSSGGLYSLSVVTVVSSSLGQTIVICNVNHPKSNVTKVDKVEPKSCDKHTHTCPCPAPE	235		
QY	238	LLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRE	297		
Db	236	LLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRE	295		
QY	298	EQNSTYRVRVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP	357		
Db	296	EQYASTYRVRVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP	355		





PCT-US02-11853-20

Query Match 93.1%; Score 2245; DB 1; Length 468;  
Best Local Similarity 93.2%; Pred. No. 4.7e-110;  
Matches 422; Conservative 10; Mismatches 15; Indels 6; Gaps 2;

QY 1 QYLVQSGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 60  
DB 20 EVLVESGGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 79  
QY 61 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 118  
DB 80 SDNVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCVRYDHYSGS-----SDYWGQGLTVT 135  
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 178  
DB 136 VSSASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 195  
QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPREPQVYTLPPS 238  
DB 196 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPREPQVYTLPPS 255  
QY 239 LGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298  
DB 256 LGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 315  
QY 299 QYNSTRYRVSVTLVHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
DB 316 QYNSTRYRVSVTLVHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 375  
QY 359 RDELTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418  
DB 376 RDELTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 435  
QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451  
DB 436 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 468  
RESULT 5  
PCT-US02-21323-12  
; Sequence 12, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: humanized 266 antibody preferred heavy chain  
PCT-US02-21323-12

Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred. No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
QY 1 QYLVQSGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 60  
DB 1 EVLVESGGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 60

QY 61 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120  
DB 61 PDTVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCASG-----DYWGQGLTVTVS 111  
QY 121 SASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 180  
DB 112 SASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 171  
QY 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
DB 172 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 231  
QY 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300  
DB 232 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 291  
QY 301 NSTYRVSVTLVHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
DB 292 NSTYRVSVTLVHODWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 351  
QY 361 ELTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 420  
DB 352 ELTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 411  
QY 421 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451  
DB 412 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 442  
RESULT 6  
PCT-US02-21324-12  
; Sequence 12, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/313,576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/383,581  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: Humanized antibody 266 preferred heavy chain variable  
PCT-US02-21324-12  
Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred. No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
QY 1 QYLVQSGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 60  
DB 1 EVLVESGGGLVQPGGSLRLSCASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSY 60  
QY 61 ADVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTVS 120  
DB 61 PDTVKGRTISRDNKNTLYLQMNLSRAEDTAVYYCASG-----DYWGQGLTVTVS 111  
QY 121 SASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 180  
DB 112 SASTKGPSVFPLAPSSKSTSGGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 171  
QY 181 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

Db 172 SGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPPELLG 231  
Qy 241 GPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 300  
Db 232 GPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 291  
Qy 301 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
Db 292 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 351  
Qy 361 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420  
Db 352 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 411  
Qy 421 WOQGNFSCSVMHAEALHNHYTKQSLSPGK 451  
Db 412 WOQGNFSCSVMHAEALHNHYTKQSLSPGK 442  
RESULT 7  
PCT-US02-26321-12  
; Sequence 12, Application PC/TUS0226321  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY  
; TITLE OF INVENTION: ASSAY METHOD FOR ALZHEIMER'S DISEASE  
; FILE REFERENCE: 8792/292  
; CURRENT APPLICATION NUMBER: PCT/US02/26321  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/334, 987  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/313, 221  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/313, 224  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: HUMANIZED ANTIBODY HEAVY CHAIN  
PCT-US02-26321-12  
Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60  
Db 1 EVQLVESGGGLVOPGGSLRLSCAASGFTFRSRYSMGWVROAPGKGLVLAQINSYGNSTYY 60  
Qy 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTVS 120  
Db 61 PDTVKGRTISRDNKNTLYLQNSLRADTAIVYCAASG-----DYWGQGLTVTVS 111  
Qy 121 SASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFAVLQS 180  
Db 112 SASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTPFAVLQS 171  
Qy 181 SGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPPELLG 240  
Db 172 SGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPPELLG 231  
Qy 241 GPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 300  
Db 232 GPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 291

Qy 301 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
Db 292 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 351  
Qy 361 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420  
Db 352 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 411  
Qy 421 WOQGNFSCSVMHAEALHNHYTKQSLSPGK 451  
Db 412 WOQGNFSCSVMHAEALHNHYTKQSLSPGK 442  
RESULT 8  
US-09-791-537-118979  
; Sequence 118979, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 118979  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-118979  
Query Match 92.5%; Score 2229.5; DB 5; Length 477;  
Best Local Similarity 91.5%; Pred No. 3.1e-109;  
Matches 422; Conservative 10; Mismatches 16; Indels 13; Gaps 2;  
Qy 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60  
Db 20 QVQLVESGGGVQVQGRSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 79  
Qy 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAKHTGGVWDP-----IDY 110  
Db 80 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAARE---GRWVRYTITTTIGYIFDY 136  
Qy 111 WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
Db 137 WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 196  
Qy 171 VHTFPVQLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 230  
Db 197 VHTFPVQLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 256  
Qy 231 PPCPAPELLGGPSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHN 290  
Db 257 PPCPAPELLGGPSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHN 316  
Qy 291 AKTPREEOYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREP 350  
Db 317 AKTPREEOYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREP 376  
Qy 351 QVYTLPPSRBELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFL 410  
Db 377 QVYTLPPSRBELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSDGSPFL 436  
Qy 411 YSKLTVDKSRWQGNFSCSVMHAEALHNHYTKQSLSPGK 451  
Db 437 YSKLTVDKSRWQGNFSCSVMHAEALHNHYTKQSLSPGK 477  
RESULT 9  
PCT-US02-21323-21  
; Sequence 21, Application PC/TUS0221323

GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: heavy chain antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (57)..(57)  
; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that if Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
; OTHER INFORMATION: ition 57 is neither Asp nor Pro and Xaa at position 56 is not Asn  
; OTHER INFORMATION: Thr, then Xaa at position 56 is not Asn  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (56)..(56)  
; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that if Xaa at position 57 is Ser or Thr, then Xaa at position 58 is Ser or Thr  
; OTHER INFORMATION: ition 57 is neither Asp nor Pro and Xaa at position 56 is not Asn  
; OTHER INFORMATION: Thr, then Xaa at position 56 is not Asn  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (58)..(58)  
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at position 57 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
; OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr  
PCT-US02-21323-21

Query Match 92.3%; Score 2226.5; DB 1; Length 442;  
Best Local Similarity 93.3%; Pred. No. 4.2e-109;  
Matches 421; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

Qy	1	QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSIGSGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMWVRQAPGKGLVLAQINSVGXXXYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYYCAKHGGVWDPIDWGOGTLVTVS	120
Db	61	PDTVKGRFTISRDNKNTLYLQMSRLRAEDTAVYYCAG-----DYWGOGTLVTVS	111
Qy	121	SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS	180
Db	112	SASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS	171
Qy	181	SGLYSLSSVTVVPSSSLGQTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLG	240
Db	172	SGLYSLSSVTVVPSSSLGQTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLG	231
Qy	241	GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQY	300
Db	232	GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQY	291
Qy	301	NSITRVVSLTVLQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRD	360
Db	292	NSITRVVSLTVLQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRD	351
Qy	361	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR	420
Db	352	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR	411

Qy	421	WQGNVFCSCVMHEALHNHYTKQSLSPGK	451
Db	412	WQGNVFCSCVMHEALHNHYTKQSLSPGK	442

RESULT 10  
PCT-US02-21324-21  
; Sequence 21, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA TO T  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/383,576  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (56)..(56)  
; OTHER INFORMATION: Xaa at position 56 is any amino acid provided that if Xaa at p  
; OTHER INFORMATION: tion 57 is neither Asp nor Pro and Xaa at position 59 is Ser o  
; OTHER INFORMATION: hr, then Xaa at position 56 is not Asn  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: heavy chain antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (57)..(57)  
; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that if Xaa at  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa  
; OTHER INFORMATION: position 57 is Asp or Pro  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (58)..(58)  
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 57 is neither Asp nor Pro,  
; OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr  
PCT-US02-21324-21

Query Match 92.3%; Score 2226.5; DB 1; Length 442;  
Best Local Similarity 93.3%; Pred. No. 4.2e-109;  
Matches 421; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

Qy	1	QVQLVSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWSIGSGSTYY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMWVRQAPGKGLVLAQINSVGXXXYY	60
Qy	61	ADSVKGRFTISRDNKNTLYLQMSRLRAEDTAVYYCAKHGGVWDPIDWGOGTLVTVS	120
Db	61	PDTVKGRFTISRDNKNTLYLQMSRLRAEDTAVYYCAG-----DYWGOGTLVTVS	111
Qy	121	SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS	180
Db	112	SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS	171
Qy	181	SGLYSLSSVTVVPSSSLGQTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLG	240
Db	172	SGLYSLSSVTVVPSSSLGQTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPCPAPPELLG	231
Qy	241	GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQY	300
Db	232	GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVVHNAKTKPREEQY	291

QY 301 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPTEKTISKAKGPREPQVYTLPPSRD 360  
 DB 292 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPTEKTISKAKGPREPQVYTLPPSRD 351  
 QY 361 ELTKNQVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDKSR 420  
 DB 352 ELTKNQVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDKSR 411  
 QY 421 WQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
 DB 412 WQGNVFCSCVMHEALHNHYTKQSLSPGK 442  
 RESULT 11  
 PCT-US02-26321-16  
 ; Sequence 16, Application PC/TUS0226321  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELI LILLY AND COMPANY AND WASHINGTON UNIVERSITY  
 ; TITLE OF INVENTION: ASSAY METHOD FOR ALZHEIMER'S DISEASE  
 ; FILE REFERENCE: 8792/292  
 ; CURRENT APPLICATION NUMBER: PCT/US02/26321  
 ; CURRENT FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: 60/334,987  
 ; PRIOR FILING DATE: 2001-10-23  
 ; PRIOR APPLICATION NUMBER: 60/313,221  
 ; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: 60/313,224  
 ; PRIOR FILING DATE: 2001-08-17  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 16  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Humanized Antibody  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(442)  
 ; OTHER INFORMATION: Humanized Antibody Heavy Chain  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (56)..(56)  
 ; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that Xaa at position 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr  
 ; OTHER INFORMATION: on 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr  
 ; OTHER INFORMATION: , then Xaa at position 56 is not Asn  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (57)..(57)  
 ; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
 ; OTHER INFORMATION: position 57 is Asp or Pro  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (58)..(58)  
 ; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that Xaa at position 56 is Asn and Xaa at position 57 is neither Asp nor Pro, then Xaa at position 58 is neither Ser nor Thr  
 ; OTHER INFORMATION: then Xaa at position 58 is neither Ser nor Thr  
 PCT-US02-26321-16  
 Query Match 92.3%; Score 2226.5; DB 1; Length 442;  
 Best Local Similarity 93.3%; Pred. No. 4.2e-109;  
 Matches 421; Conservative 7; Mismatches 14; Indels 9; Gaps 1;  
 QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTVY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTVY 60  
 QY 61 ADSVKGRTISDKNLTLLQMNLSRAEDTAVYCAKHTGGVWDPIYWCQGLTVTS 120  
 DB 61 PDTVKGRTISDKNLTLLQMNLSRAEDTAVYCAKHTGGVWDPIYWCQGLTVTS 111

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 180  
 DB 112 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 171  
 QY 181 SGLYSLSVVVPSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCTCPCPAPPELLG 240  
 DB 172 SGLYSLSVVVPSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCTCPCPAPPELLG 231  
 QY 241 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENYVDGVEVHNAKTKPREEQY 300  
 DB 232 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENYVDGVEVHNAKTKPREEQY 291  
 QY 301 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPTEKTISKAKGPREPQVYTLPPSRD 360  
 DB 292 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPTEKTISKAKGPREPQVYTLPPSRD 351  
 QY 361 ELTKNQVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDKSR 420  
 DB 352 ELTKNQVSLTCLVKGFPDIAVWESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDKSR 411  
 QY 421 WQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
 DB 412 WQGNVFCSCVMHEALHNHYTKQSLSPGK 442  
 RESULT 12  
 US-10-206-008-645  
 ; Sequence 645, Application US/10206008  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PTZ53C1N  
 ; CURRENT APPLICATION NUMBER: US/10/206,008  
 ; CURRENT FILING DATE: 2002-07-29  
 ; PRIOR APPLICATION NUMBER: 09/760,479  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: 60/179,065  
 ; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: 60/180,628  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: 60/214,886  
 ; PRIOR FILING DATE: 2000-06-28  
 ; PRIOR APPLICATION NUMBER: 60/217,487  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 60/225,758  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/220,963  
 ; PRIOR FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: 60/217,496  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 60/225,447  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/218,290  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/225,757  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/226,868  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 60/216,647  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: 60/225,267  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/216,880  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: 60/225,270  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/251,869  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: 60/235,834  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: 60/234,274  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: 60/234,223

1	PRIOR FILING DATE: 2000-09-21
2	PRIOR APPLICATION NUMBER: 60/228,924
3	PRIOR FILING DATE: 2000-08-30
4	PRIOR APPLICATION NUMBER: 60/224,518
5	PRIOR FILING DATE: 2000-08-14
6	PRIOR APPLICATION NUMBER: 60/236,369
7	PRIOR FILING DATE: 2000-09-29
8	PRIOR APPLICATION NUMBER: 60/224,519
9	PRIOR FILING DATE: 2000-08-14
10	PRIOR APPLICATION NUMBER: 60/220,964
11	PRIOR FILING DATE: 2000-07-26
12	PRIOR APPLICATION NUMBER: 60/241,809
13	PRIOR FILING DATE: 2000-10-20
14	PRIOR APPLICATION NUMBER: 60/249,299
15	PRIOR FILING DATE: 2000-11-17
16	PRIOR APPLICATION NUMBER: 60/236,327
17	PRIOR FILING DATE: 2000-09-29
18	PRIOR APPLICATION NUMBER: 60/241,785
19	PRIOR FILING DATE: 2000-10-20
20	PRIOR APPLICATION NUMBER: 60/244,617
21	PRIOR FILING DATE: 2000-11-01
22	PRIOR APPLICATION NUMBER: 60/225,268
23	PRIOR FILING DATE: 2000-08-14
24	PRIOR APPLICATION NUMBER: 60/236,368
25	PRIOR FILING DATE: 2000-09-29
26	PRIOR APPLICATION NUMBER: 60/251,856
27	PRIOR FILING DATE: 2000-12-08
28	PRIOR APPLICATION NUMBER: 60/251,868
29	PRIOR FILING DATE: 2000-12-08
30	PRIOR APPLICATION NUMBER: 60/229,344
31	PRIOR FILING DATE: 2000-09-01
32	PRIOR APPLICATION NUMBER: 60/234,997
33	PRIOR FILING DATE: 2000-09-25
34	PRIOR APPLICATION NUMBER: 60/229,343
35	PRIOR FILING DATE: 2000-09-01
36	PRIOR APPLICATION NUMBER: 60/229,345
37	PRIOR FILING DATE: 2000-09-01
38	PRIOR APPLICATION NUMBER: 60/229,287
39	PRIOR FILING DATE: 2000-09-01
40	PRIOR APPLICATION NUMBER: 60/229,513
41	PRIOR FILING DATE: 2000-09-05
42	PRIOR APPLICATION NUMBER: 60/231,413
43	PRIOR FILING DATE: 2000-09-08
44	PRIOR APPLICATION NUMBER: 60/229,509
45	PRIOR FILING DATE: 2000-09-05
46	PRIOR APPLICATION NUMBER: 60/236,367
47	PRIOR FILING DATE: 2000-09-29
48	PRIOR APPLICATION NUMBER: 60/237,039
49	PRIOR FILING DATE: 2000-10-02
50	PRIOR APPLICATION NUMBER: 60/237,038
51	PRIOR FILING DATE: 2000-10-02
52	PRIOR APPLICATION NUMBER: 60/236,370
53	PRIOR FILING DATE: 2000-09-29
54	PRIOR APPLICATION NUMBER: 60/236,802
55	PRIOR FILING DATE: 2000-10-02
56	PRIOR APPLICATION NUMBER: 60/237,037
57	PRIOR FILING DATE: 2000-10-02
58	PRIOR APPLICATION NUMBER: 60/237,040
59	PRIOR FILING DATE: 2000-10-02
60	PRIOR APPLICATION NUMBER: 60/240,960
61	PRIOR FILING DATE: 2000-10-20
62	PRIOR APPLICATION NUMBER: 60/239,935
63	PRIOR FILING DATE: 2000-10-13
64	PRIOR APPLICATION NUMBER: 60/239,937
65	PRIOR FILING DATE: 2000-10-13
66	PRIOR APPLICATION NUMBER: 60/241,787
67	PRIOR FILING DATE: 2000-10-20
68	PRIOR APPLICATION NUMBER: 60/246,474
69	PRIOR FILING DATE: 2000-11-08
70	PRIOR APPLICATION NUMBER: 60/246,532
71	PRIOR FILING DATE: 2000-11-08
72	PRIOR APPLICATION NUMBER: 60/249,216
73	PRIOR FILING DATE: 2000-11-17

1	PRIOR APPLICATION NUMBER: 60/249,211
2	PRIOR FILING DATE: 2000-11-17
3	PRIOR APPLICATION NUMBER: 60/226,681
4	PRIOR FILING DATE: 2000-08-22
5	PRIOR APPLICATION NUMBER: 60/225,759
6	PRIOR FILING DATE: 2000-08-14
7	PRIOR APPLICATION NUMBER: 60/225,213
8	PRIOR FILING DATE: 2000-08-14
9	PRIOR APPLICATION NUMBER: 60/227,182
10	PRIOR FILING DATE: 2000-08-22
11	PRIOR APPLICATION NUMBER: 60/225,214
12	PRIOR FILING DATE: 2000-08-14
13	PRIOR APPLICATION NUMBER: 60/235,836
14	PRIOR FILING DATE: 2000-09-27
15	PRIOR APPLICATION NUMBER: 60/230,438
16	PRIOR FILING DATE: 2000-09-06
17	PRIOR APPLICATION NUMBER: 60/215,135
18	PRIOR FILING DATE: 2000-06-30
19	PRIOR APPLICATION NUMBER: 60/225,266
20	PRIOR FILING DATE: 2000-08-14
21	PRIOR APPLICATION NUMBER: 60/249,218
22	PRIOR FILING DATE: 2000-11-17
23	PRIOR APPLICATION NUMBER: 60/249,208
24	PRIOR FILING DATE: 2000-11-17
25	PRIOR APPLICATION NUMBER: 60/249,213
26	PRIOR FILING DATE: 2000-11-17
27	PRIOR APPLICATION NUMBER: 60/249,212
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29	PRIOR APPLICATION NUMBER: 60/249,207
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33	PRIOR APPLICATION NUMBER: 60/249,244
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35	PRIOR APPLICATION NUMBER: 60/249,217
36	PRIOR FILING DATE: 2000-11-17
37	PRIOR APPLICATION NUMBER: 60/249,211
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39	PRIOR APPLICATION NUMBER: 60/249,215
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44	PRIOR FILING DATE: 2000-11-17
45	PRIOR APPLICATION NUMBER: 60/249,297
46	PRIOR FILING DATE: 2000-11-17
47	PRIOR APPLICATION NUMBER: 60/232,400
48	PRIOR FILING DATE: 2000-09-14
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51	PRIOR APPLICATION NUMBER: 60/232,081
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53	PRIOR APPLICATION NUMBER: 60/232,080
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58	PRIOR FILING DATE: 2000-09-08
59	PRIOR APPLICATION NUMBER: 60/233,064
60	PRIOR FILING DATE: 2000-09-14
61	PRIOR APPLICATION NUMBER: 60/233,063
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63	PRIOR APPLICATION NUMBER: 60/232,397
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65	PRIOR APPLICATION NUMBER: 60/232,399
66	PRIOR FILING DATE: 2000-09-14
67	PRIOR APPLICATION NUMBER: 60/232,401
68	PRIOR FILING DATE: 2000-09-14
69	PRIOR APPLICATION NUMBER: 60/241,808
70	PRIOR FILING DATE: 2000-10-20
71	PRIOR APPLICATION NUMBER: 60/241,826
72	PRIOR FILING DATE: 2000-10-20
73	PRIOR APPLICATION NUMBER: 60/241,786

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match          92.3%; Score 2224.5; DB 6; Length 499;
Best Local Similarity 91.9%; Pred. No. 6e-109;
Matches 421; Conservative 13; Mismatches 17; Indels 7; Gaps 2;

Qy 1 QVQLVQSGGGLVQPGGSLRLCSAASGFTFRSNAMGWTRQAPGKLEWVSGISGSGSIYY 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 42 QAQLVSGGGLVQPGGSLRLCSASGFTFSDNYMSWIRQAPGKLEWVSYISCSGETIYY 101
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA---KHTGGGVWDPIDY---WGQ 113
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 102 GDSVGRGFTISRDNKQSLYLQMSLSRADDTAVYYCARERRYCGGGFYLDHYGMDVMWQ 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 114 GTLVTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPPPTVSNNSGALTSGVHT 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 GTTVTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPPPTVSNNSGALTSGVHT 221
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 174 FPAVLQSSGLYSLSSVTVVSSSLGTQYICNVNHRKSNLKVDKPKVPSKCDKTHTCPPC 233
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 222 FPAVLQSSGLYSLSSVTVVSSSLGTQYICNVNHRKSNLKVDKPKVPSKCDKTHTCPPC 281
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 234 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAT 293
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 282 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAT 341
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 294 KPREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTSKAKGPREPQVY 353
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 342 KPREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTSKAKGPREPQVY 401
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 354 TLPSPRDELTKNOVSLTCLVKGFPYSDTAVESNGQFPENNYKTTTPVLDSDGSGFFLSK 413
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 402 TLPSPRDELTKNOVSLTCLVKGFPYSDTAVESNGQFPENNYKTTTPVLDSDGSGFFLSK 461
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 414 LTVDKSRWQGNVFCFSVNHAEALHNHYTKLSLSLSPGK 451
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 462 LTVDKSRWQGNVFCFSVNHAEALHNHYTKLSLSLSPGK 499
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-10-206-008-636
; Sequence 636, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT#53CIN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,213  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 92.2%; Score 2223.5; DB 6; Length 494;

Best Local Similarity 93.0%; Pred No. 6.6e-109;  
Matches 422; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

Qy 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGVHVRQAPGKGLWVSGISGGSGTYY 60  
Db 41 EVQLVESGGGLVPGGSLRLSCAAAEFAFENYMMHWVRQAPGKGLWVSHLSDGSSTRY 100  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAREDVAVYCAK--HTGGGVDP-IDYWGQGLV 117  
Db 101 ADSVKGRFTISRDNKNTLYLQMSLRVEDVAVYCARVKGTGSSWSPDFDYGQGLV 160  
Qy 118 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 177  
Db 161 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 220  
Qy 178 LQSSGLYSLSSVTVPSSSLSGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPCPAPE 237  
Db 221 LQSSGLYSLSSVTVPSSSLSGTQTYICNVNHPKSNFKVDKVEPKSCDKTHTCPCPAPE 280  
Qy 238 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPRE 297  
Db 281 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPRE 340  
Qy 298 EQYNSTYRVYSVLTVLDHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 357  
Db 341 EQYNSTYRVYSVLTVLDHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 400  
Qy 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFFLYSKLIVD 417  
Db 401 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFFLYSKLIVD 460  
Qy 418 KSRWQGGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
Db 461 KSRWQGGNVFSCSVNHEALHNHYTQKSLSLSPGK 494

RESULT 14

US-10-089-500-53

; Sequence 53, Application US/10089500

; GENERAL INFORMATION:

; APPLICANT: KYOWA HAKKO KOGYO CO., LTD

; TITLE OF INVENTION: Humanized anti-GD3 antibody and it's cytokine conjugate

```
; FILE REFERENCE: 11239WO1
; CURRENT APPLICATION NUMBER: US/10/089,500
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: H11-278291
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein
US-10-089-500-53

Query Match          91.9%; Score 2216; DB 6; Length 582;
Best Local Similarity 92.7%; Pred. No. 1.9e-108;
Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
DB 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFASHYAMSVROAPGKGLWVAYISSGGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 61 SDVKGRFTISRDNKNTLYLQMNLSRAEDSAVYFCTRVKLGTY--FDSWGQGLTVTS 118
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
DB 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 178
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCCPCPAPELLG 240
DB 179 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCCPCPAPELLG 238
QY 241 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300
DB 239 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 298
QY 301 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360
DB 299 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 358
QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420
DB 359 ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 418
QY 421 WQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
DB 419 WQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

RESULT 15
US-09-304-465A-2
; Sequence 2, Application us/09304465A
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/09/304,465A
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-304-465A-2
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Query Match          91.8%; Score 2214.5; DB 5; Length 449;
Best Local Similarity 92.7%; Pred. No. 1.8e-108;
Matches 417; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLWVSGISGGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWYRQAPGKGLWVARIYPTNGYTRY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCSRWGGDGFY-AMDYWGQGLTVTS 119
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
DB 120 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCCPCPAPELLG 240
DB 180 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCCPCPAPELLG 239
QY 241 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300
DB 240 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 299
QY 301 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360
DB 300 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 359
QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420
DB 360 EMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 419
QY 421 WQOGNVFSCSVNHEALHNHYTQKSLSLSPG 450
DB 420 WQOGNVFSCSVNHEALHNHYTQKSLSLSPG 449
```

Search completed: October 9, 2002, 19:21:24  
Job time : 60.8265 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 24.1607 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1767	73.3	330	1 GHU	Ig gamma-1 chain C
2	1630.5	67.6	377	2 A23511	Ig gamma-3 chain C
3	1628.5	67.5	377	2 A60764	Ig gamma-3 chain C
4	1604	66.5	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	66.0	327	1 G4HU	Ig gamma-4 chain C
6	1513	62.8	470	2 G22080	Ig heavy chain pre
7	1499.5	62.2	444	2 FC4436	monoclonal antibody
8	1451.5	60.2	469	2 S37483	Ig gamma-2a chain
9	1435	59.5	446	2 S40295	Ig gamma-2a chain
10	1433	59.4	374	2 S69339	Ig heavy chain V r
11	1430	59.3	472	2 S31459	Ig gamma-1 chain -
12	1382	57.3	474	1 G2MS11	Ig gamma-2b chain
13	1376.5	57.1	475	2 S01321	Ig gamma-2b chain
14	1263	52.4	328	2 I47159	Ig gamma-2a chain
15	1260	52.3	255	4 S31866	Ig gamma-1 chain C
16	1257	52.1	328	2 I47160	Ig gamma-2b chain
17	1254	52.0	234	2 PT0207	Ig gamma chain C r
18	1231	51.1	328	2 I47158	Ig gamma-1 chain C
19	1230.5	51.0	323	1 GHRB	Ig gamma chain C r
20	1227	50.9	328	2 I47161	Ig gamma-3 chain C
21	1216.5	50.5	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	48.2	308	2 C30554	Ig heavy chain C r
23	1152	47.8	326	2 FS0017	Ig gamma-1 chain C
24	1151	47.7	289	1 G3HUW1	Ig gamma-1 chain c
25	1146.5	47.6	333	2 FS0018	Ig gamma-2b chain
26	1142	47.4	324	1 G1MS	Ig gamma-1 chain C
27	1141	47.3	329	1 G3MSC	Ig gamma-3 chain C
28	1137	47.2	393	1 G1MSM	Ig gamma-1 chain C
29	1130	46.9	398	1 G3MSM	Ig gamma-3 chain C

## ALIGNMENTS

## RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C:Accession: A93433; S38861; S3887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaudo, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113/235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammagamma-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammagamma-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni



Query Match	67.5%;	Score 1628.5;	DB 2;	Length 377;
Best Local Similarity	82.0%;	Pred. No. 1.5e-86;		
Matches 309;	Conservative 10;	Mismatches 11;	Indels 47;	Gaps

  

QY	122	ASTKGPSVFPLPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	181
DB	1	ASTKGPSVFPLPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60
QY	182	GLYSLSVVVVPSSLSGTQTYICNVNHKPSNTKVDKKY-----	219
DB	61	GLYSLSVVVVPSSLSGTQTYICNVNHKPSNTKVDKRVELKTLPLGDTHTCPRCPEPKGC	120
QY	220	-----EPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDT	254
DB	121	DTTPPCPRCPKPKSCDTPPCPRCPKPKSCDTPPCPRCPAPELLGGPSVFLPPKPKDT	180
QY	255	LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLI	314
DB	181	LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLI	240
QY	315	QDWLNGKEYKCKVSNKALPAPIEKTLSKAAGQPREPQVYTLTPSRDRLTAKNOVSLCIVK	374
DB	241	QDWLNGKEYKCKVSNKALPAPIEKTLSKTKGQPREPQVYTLTPSRDRLTAKNOVSLCIVK	300
QY	375	GFYPSDIAVEWESNGQPENNYKTTTPVLVDSGSFFLYSKLTVDKSRWQQGNVSCSVMHE	434
DB	301	GFYPSDIAVEWESNGQPENNYNTTPVLVDSGSFFLYSRLTVDKSRWQEGNVSCSVMHE	360
QY	435	ALHNHYTQKSLSVSPGK	451
DB	361	ALHNRTQKLSLSVSPGK	377

A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; #le, revisions to residues 25, 59, 60, and 264-268  
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amid  
ned

B:Milstein, C.; Frangione, B.  
Biochem. J. 121 217-225, 1971  
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:l19338; OMIM:147110  
A:Map position: 1432.33-1432.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/disulfide bonds: #status experimental  
F:102,103,106,109/disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.5%; Score 1604; DB 1; Length 326;  
Best Local Similarity 91.2%; Pred. No. 3.3e-85;  
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

Qy 122 ASTKGSPVFLPAPSKSTSGSTAALGCLVLKDYFPPEPTVSWSNGALTSGVHTFFPAVLQSS 181  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 ASYTKGPSVPPLAPCSRSTSESTAALGCLVLKDYFPPEPTVSWSNGALTSGVHTFFPAVLQSS 60  
  
Qy 182 GLYSLSGVTVTPSSISGTQTYTCNNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPELLGG 241  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 GLISLSGVTVTPSSNFGITTYTCNDVHPNSNKVDKTIKERKCVE--CPPCPAPP-VAG 116  
  
Qy 242 PSVELPPPKPKDTLMISRTEPYTCVVVDVSHEDDEVFKFNMYVDGVEVHNAKTKPREEQYN 301  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 117 PSVELPPPKPKDTLMISRTEPYTCVVVDVSHEDDEVFNMYVDGVEVHNAKTKPREEQFN 176  
  
Qy 302 STTRVSVLTFLHDWLNGKEYCKVKSNKALPAPIETKTISKAKGPREFOVYTLPPSRDE 361  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 177 STRVSVLTFLVHQDWLNGLKEYCKVKSNKGLPAPIETKTISKTKQPREFOVYTLPPSREE 236  
  
Qy 362 LTKNQVSLTCLVKGFYPSDIAEVWESNQPENNYTKTTPPVLDSDGSFFLYSKLTVDKSRW 421  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 237 MTNQVSLTCLVKGFYPSDIAEVWESNQPENNYTKTTPPMILDSGDSFFLYSKLTVDKSRW 296  
  
Qy 422 QCGNVFSCSMHEALHNHYTQKSLSLSPGK 451  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 297 QCGNVFSCSMHEALHNHYTQKSLSLSPGK 326

RESULT 5  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150  
R:Elliison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104

A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <EL>  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region  
A:Reference number: A30249; MUID:70207560  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
C:Genetics:  
A:Gene: IGHG4  
A:Cross-references: GDB:119340; OMTM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 95/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.0%; Score 1590.5; DB 1; Length 327;  
Best Local Similarity 90.9%; Pred. No. 2e-84;  
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 122 ASKGPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 181  
DB 1 ASKGPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVTVLHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 241  
DB 61 GLYSLSVTVLHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 117

QY 242 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVAFNMFVDCGEVHNNAKTPREEQV 301  
DB 118 PSVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVAFNMFVDCGEVHNNAKTPREEQV 177

QY 302 STYRVSVTLVHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 361  
DB 178 STYRVSVTLVHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 237

QY 362 LTRNQVSLCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSFLLYSLKLTVDKSRW 421  
DB 238 MTRNQVSLCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSFLLYSLKLTVDKSRW 297

QY 422 QGNVFSVCSVMHEALHNHYTKQSLSPGK 451  
DB 298 QGNVFSVCSVMHEALHNHYTKQSLSPGK 327

RESULT 6  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A:Accession: S22080; S06610; A31303  
R:Sanders, P. G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g  
A:Reference number: S06610; MUID:90079556  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: EMBL:X16701  
A:Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Gene: Ig CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 1513; DB 2; Length 470;  
Best Local Similarity 64.2%; Pred. No. 8.3e-80;  
Matches 292; Conservative 55; Mismatches 100; Indels 8; Gaps 6;

QY 1 QVQLVDSGGGLVOPGGSLRLSCAASGFTFRSNAMGVRAQAPKGLVWVSGISGGSTYY 60  
DB 20 QVQLRESGSPSLVKPSQTLTCTVSGFSLSYALTFRQAPKALEWVGIT-SGGTTY 78

QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVMDP--IDYMGQGTLYT 118  
DB 79 NPALKSRLSITKENSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAMGGLLVT 138

QY 119 VSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVL 178  
DB 139 VSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVL 198

QY 179 QSSGLYSLSVTVLHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 238  
DB 199 QSSGLYSLSVTVLHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 255

QY 239 LGSPVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVAFNMFVDCGEVHNNAKTPREE 298  
DB 256 LGSPVFLPPPKPDKTLMISRTPEVTCVVDVSHEDPEVAFNMFVDCGEVHNNAKTPREE 315

QY 299 QYNTSTYRVSVTLVHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 358  
DB 316 QYNTSTYRVSVTLVHQLWLNKGEYKCKVSNKALPAPAEIKTISKAKQPREQVYLPSPRDE 375

QY 359 RDELTRNQVSLCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSFLLYSLKLTVDK 416  
DB 376 RDELTRNQVSLCLVKGFPYPSDIAVWESNGQPNNTKTPPVLDSDGSFLLYSLKLTVDK 435

QY 417 DKSRWQGNVFSVCSVMHEALHNHYTKQSLSPGK 451  
DB 436 DKSRWQGNVFSVCSVMHEALHNHYTKQSLSPGK 470

RESULT 7  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp  
A:Reference number: JC5810; MUID:98063277  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted



[illegible]

Db 341 KSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 374

RESULT 11

S31459

Ig gamma-1 chain - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999

C:Accession: S31459

R:Patrici, S.; Nau, F.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31459

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-472 <PAT>

A:Cross-references: EMBL:X69797

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 1430; DB 2; Length 472;

Best Local Similarity 59.7%; Pred. No. 4.9e-75;

Matches 273; Conservative 63; Mismatches 113; Indels 8; Gaps 4;

QY 1 QVOLVSGGGLVPGGSLRSLCAASGFTFRSNAGWVRQAPGKLEWVSGISGGSTYY 60

DB 18 QVRLEGSGSLATLLQTLSTVCTISGFLNNGYGVWVRQAPGKALEWLG-SGYDEDDY 76

QY 61 ADSVKGFTISRDNKNTLYLQMSLRAEDTAVYYCAK----HTGGGVMDPIDYWGQGL 116

DB 77 NPVLKSLRSLTKDTSKQSVLTLSTVTDYAVYCARVDYDSSHAFAAYSYDFWGPGLL 136

QY 117 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWMNSGALTSGVHTFPA 176

DB 137 ISVLASSTTPPKVPLTSCCGDTSSIVTLGCLVSSYMPPEPTVTSWMNSGALTSGVHTFPA 196

QY 177 VLASSGLYLSVVTVPPSSSLGTQTYICNNVHNPSTNFKVDKVEPKSCDTHTCPPCAP 236

DB 197 ILOSSGLYLSVVTVPPASTVPASTGQTFICNVAHPASSTFKVDKRVPEGCPDCKHC-RCPPP 255

QY 237 ELLGGPSVFLPPPKPDTLMISRTEPTVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296

DB 256 ELPGPSVFIFPPKPKDTLIISGTPEVTCVVVDVQDDPEVQFSWFVDNVEVRTATKPR 315

QY 297 EEQYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356

DB 316 EEQPNSTFRVVSALPQHQDWLGGKEFKCKVHNALPAPIVRTISRTKGOAREPQVYVLA 375

QY 357 PSRDELTKNQLSFLCLVKGFYPSDIAVEWESNGQP--ENNYKTTPTPVLDSGDSFFLYSKL 414

DB 376 PPQELSKEKSLSVLCVLVGTGFYPDYIAVEWKNQGPESDEKYGTTTSQILDAGSYFLYSRL 435

QY 415 TVDKSRQQGNVFCSCVMHEALHNHYTKQSLSLSPGK 451

DB 436 RVDKNSMQEGDTYACVVMHEALHNHYTKQSLSPGK 472

RESULT 12

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000

C:Accession: S25057; A02157; A26235; A26233; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munsziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAAA7649.1; PID:g54827

Db 137 AAKTTPSVYPLAPCGDGTGSSVTSGCLVKGYFPSPVTVTWNSGSLSSSVHTLSQALLQ 4133

Qy 181 SGLYSLSSVTVFPSSLSGTQTYICNVNHNKPSNTKVDKPEKSCDKT-HTCPP-----C 2333

Db 197 SGLYTWSSSVTVFPSSVTWPSTQVTCVAHPASSTVVDKLEPSPGPTSTINPCPKCKECHK 2556

Qy 234 PAPELGGPSVFLFPKPKDITLMSRTPPEVTCVVVDVSHEDPEVKFNMYVDGVVHNAKT 2933

Db 257 PAPNLGGGSPVFFPPNLIKDVMLSLTPKTVCVVDVSEDDPDVQLISFWVNNVEVHTAQT 3116

Qy 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKQGPPEQVY 3535

Db 317 QTHREDYNSTIRVWSVLTPIQHDWMSGKEPKCKVNNKNDLPSPERTISKIKGLVRAPQVY 3767

Qy 354 TLPSPSDELTKNQVSLTCLVLKGFYPSDIAVDEWSNGQPNNTKPTPVLDSDGSEFFLYSK 4133

Db 377 ILPPAPRAQLSKDVSLTCLVLGVFPNGDISVETWNSGHTENTKDTAPVLDSGDSFYFSK 4366

Qy 414 LTVDKSRWQGNVFCSCVMYHEALHNHYTQKSLSLSPGK 451

Db 437 LNMKTSEKWTDSFCNVREHGLKNYLLKKTISRSPGK 474

RESULT 13

SOL1321

Ig gamma-2b chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999

C:Accession: SOL1321

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin

A:Reference number: SOL1320; MUID:88329081

A:Accession: SOL1321

A:Molecule type: mRNA

A:Residues: 1-475 <DE>

A:Cross-references: EMBL:X13188; MID:g51780; PIDR:CAA31580.1; PID:g51781

A:Note: This sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>

F:139-223/Domain: immunoglobulin homology <IMH>

Query Match 57.1%; Score 1376.5; DB 2; Length 475;

Best Local Similarity 57.2%; Pred. No. 5.8e-72;

Matches 262; Conservative 71; Mismatches 116; Indels 9; Gaps

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNGAVRQAPGKLEWYSGTISGGSTYY 60

Db 20 QVQLQSGAELARPAGSKVLSKASGYTLISGISWVKQRTGGLEWIGEITYPGSGNSYF 79

Qy 61 ADSVKGRFTISRDNKNTLYIQMNSLRADETAVYCAKHTGGGVWDPIDYWGQGLTIVTS 120

Db 80 NEKFKGKAVLTVDKSSSYAYLHLSSLTSEDSYAFYFCAGPQVGLL-PFGYWGQGLTIVTS 138

Qy 121 SASLKGPSVFELPAPSKSTSGTAAIGLVKDYKFPPEPVTVVNSGALTSVGHVTPAVLQS 180

Db 139 AAKTTPSVYPLAPCGDGTGSSVTLCGLVKGYFPSPVTVTWNSGSLSSSVHTFPALLQ- 197

Qy 181 SGLYSLSSVTVFPSSLSGTQTYICNVNHNKPSNTKVDKPEKSCDKT-HTCPP-----C 2333

Db 198 SGLYTWSSSVTVFPSSVTWPSTQVTCVAHPASSTVVDKLEPSPGPTSTINPCPKCKECHK 2557

Qy 234 PAPELGGPSVFLFPKPKDITLMSRTPPEVTCVVVDVSHEDPEVKFNMYVDGVVHNAKT 2933

Db 258 PAPNLGGGSPVFFPPNLIKDVMLSLTPKTVCVVDVSEDDPDVQLISFWVNNVEVHTAQT 3117

Qy 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKQGPPEQVY 3535

Db 318 QTHREDYNSTIRVWSVLTPIQHDWMSGKEPKCKVNNKNDLPAPIERTISKIKGLVRAPQVY 3770

Qy 354 TLPSPSDELTKNQVSLTCLVLKGFYPSDIAVDEWSNGQPNNTKPTPVLDSDGSEFFLYSK 4133

Db 378 ILSPPEQLSRKVDLSLCLAVGSPEDISVEVTSNGHTTEENYKDTAPVLDSGYSFIYSK 437  
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 438 LNMKTSKWEKTDSCNVRHEGLKNYLLKTIISRSPGK 475  
RESULT 14  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
A:Gene: IgG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 52.4%; Score 1263; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 1.2e-65;  
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;  
QY 122 ASTKGPSVFPLAPSKSTGGTAALGLVKDYFPEPTVYVSNMNGALTSVHTFPAVLQSS 181  
Db 1 APKTAPSVYPLACRDTSGPNVALGCLASSYFPEPTVYVSNMNGALSSGVHTFPAVLQPS 60  
QY 182 GLYSLSSVTVVSSSLCTQYICNVNHNKPSNTKVDKKVEPKSCDKTHCCPPCPAPPELLGG 241  
Db 61 GLYSLSSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGKTTPPCPCPCAPCESP---G 116  
QY 242 PSVELFPKPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPKREEQYN 301  
Db 117 PSVIFPPKPKKDTLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNATKPKREEQYN 176  
QY 302 STYRVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 361  
Db 177 STYRVSVLTVLHODWLNGLNGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPHAE 236  
QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGO--PENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 419  
Db 237 LRSKVSITCLVIGFYPPDIDVENQRNGQPEPEGNVYRTTPPOQVDYDGYFLYSKFSVDKA 296  
QY 420 RWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 297 SWQGGIGFQCAVMHEALHNHYTKSLSLSPGK 328  
RESULT 15  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g333068; PIDN:CAA49866.1; PID:g333069  
C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region  
Query Match 52.3%; Score 1260; DB 4; Length 255;  
Best Local Similarity 97.5%; Pred. No. 1.4e-65;  
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 213 TKVDKKVEPKSCDKTHCCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSH 272  
Db 17 TVAQADVESKSCDKTHCCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSH 76  
QY 273 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNGLNGEYKCKVSNKAL 332  
Db 77 EDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNGLNGEYKCKVSNKAL 136  
QY 333 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPE 392  
Db 137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPE 196  
QY 393 NNKYKTPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 197 NNKYKTPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 255

Search completed: October 9, 2002, 19:13:20  
Job time : 25.1607 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:54 ; Search time 13.8061 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVPGSSLR.....MHEALHNHYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	1767	73.3	330	1 GC1_HUMAN	P01857 homo sapien
2	1604	66.5	325	1 GC2_HUMAN	P01859 homo sapien
3	1590.5	66.0	327	1 GC4_HUMAN	P01861 homo sapien
4	1230.5	51.0	323	1 GC_RABIT	P01870 oryctolagus
5	1216.5	50.5	329	1 GC2_CAVPO	P01862 cavia porce
6	1156	47.9	290	1 GC3_HUMAN	P01860 homo sapien
7	1152	47.8	326	1 GC1_RAT	P20759 rattus norv
8	1146.5	47.6	333	1 GCB_RAT	P20761 rattus norv
9	1142	47.4	324	1 GC1_MOUSE	P01868 mus musculus
10	1141	47.3	329	1 GC3_MOUSE	P22436 mus musculus
11	1137	47.2	393	1 GC1M_MOUSE	P01869 mus musculus
12	1130	46.9	398	1 GC3M_MOUSE	P03987 mus musculus
13	1126	46.7	330	1 GCAA_MOUSE	P01863 mus musculus
14	1123.5	46.6	335	1 GCAB_MOUSE	P01864 mus musculus
15	1121	46.5	399	1 GCAM_MOUSE	P01865 mus musculus
16	1118.5	46.4	329	1 GCC_RAT	P20762 rattus norv
17	1112	46.1	322	1 GCA_RAT	P20760 rattus norv
18	1087	45.1	336	1 GCB_MOUSE	P01866 mus musculus
19	1082	44.9	405	1 GCBM_MOUSE	P01867 mus musculus
20	492	20.4	428	1 EPC_MOUSE	P01854 homo sapien
21	483.5	20.1	429	1 EPC_RAT	P01855 rattus norv
22	471	19.5	117	1 HV3C_HUMAN	P01764 homo sapien
23	468	19.4	421	1 EPC_MOUSE	P06336 mus musculus
24	466.5	19.3	114	1 HV3B_HUMAN	P01763 homo sapien
25	456.5	18.9	122	1 HV3G_HUMAN	P01768 homo sapien
26	450.5	18.7	122	1 HV3A_HUMAN	P01762 homo sapien
27	449.5	18.6	116	1 HV3T_HUMAN	P01781 homo sapien
28	447	18.5	121	1 HV3J_HUMAN	P01771 homo sapien
29	444	18.4	454	1 MUC_HUMAN	P01871 homo sapien
30	440	18.2	455	1 MUC_MOUSE	P01872 mus musculus
31	439	18.2	458	1 MUC_RABIT	P03988 oryctolagus
32	438.5	18.2	116	1 HV05_CARAU	P19181 carassius a
33	437.5	18.1	122	1 HV3H_HUMAN	P01769 homo sapien

34	437.5	18.1	126	1 HV3K_HUMAN	P01772 homo sapien
35	435.5	18.1	136	1 HV16_MOUSE	P01783 mus musculus
36	435	18.0	115	1 HV3D_HUMAN	P01765 homo sapien
37	432	17.9	117	1 HV02_CANFA	P01785 canis famil
38	430	17.8	476	1 MUCM_MOUSE	P01873 mus musculus
39	429	17.8	479	1 MUCM_RABIT	P04221 oryctolagus
40	428	17.8	119	1 HV3I_HUMAN	P01770 homo sapien
41	427	17.7	115	1 HV3F_HUMAN	P01767 homo sapien
42	422.5	17.5	120	1 HV3U_HUMAN	P01782 homo sapien
43	422	17.5	457	1 MUC_SUNMO	P20768 suncus muri
44	419.5	17.4	119	1 HV3M_HUMAN	P01774 homo sapien
45	419	17.4	120	1 HV3E_HUMAN	P01766 homo sapien

#### ALIGNMENTS

RESULT 1  
GC1\_HUMAN  
ID GC1\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN IGHC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RP MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from *Staphylococcus*  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE  
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 CC MARKER & THE GIM (NON-1) MARKERS.  
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC 35,116,198,269 & 272.  
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC RESIDUES 198,267&272.  
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 CC -----  
 DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A02146; GHU.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR TIM; 147100;  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_Like; 1.  
 DR SMART; SM00407; IG\_C1; 2.  
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 FT DOMAIN 1 98 CH1.  
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 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
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Qy	182	GLXSLSSVTVTPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG	241
Db	61	GLXSLSSVTVTPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKTHTCPCPAPELGG	120
Qy	242	PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN	301
Db	121	PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN	180
Qy	302	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE	361
Db	181	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE	240
Qy	362	LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	421
Db	241	LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW	300
Qy	422	QGNVFSCSVNHEALHNHYTQKSLSLSPGK	451
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RESULT 2  
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 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-2 chain C region.  
 GN IGHG2  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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RN [1] SEQUENCE OF 2-326 FROM N.A.  
 RX MEDLINE=82197621; PubMed=6804948;  
 RA Ellison J.W., Hood L.E.;  
 RT "Linkage and sequence homology of two human immunoglobulin gamma  
 heavy chain constant region genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
 RN [2]  
 RP SEQUENCE OF 88-115 FROM N.A.  
 RC TISSUE=Fetal liver;  
 RX MEDLINE=83001943; PubMed=6811139;  
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;  
 RT "Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.";  
 RL Cell 29:671-679(1982).  
 RN [3]  
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
 RC TISSUE=Fetal liver;  
 RX MEDLINE=84235992; PubMed=6329676;  
 RA Krawinkel U., Rabbitts T.H.;  
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
 genes.";  
 RL EMBO J. 1:403-407(1982).  
 RN [4]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RX MEDLINE=81007873; PubMed=6774012;  
 RA Wang A.-C., Tung E., Fudenberg H.H.;  
 RT "The primary structure of a human IgG2 heavy chain: genetic,  
 evolutionary, and functional implications.";  
 RL J. Immunol. 125:1048-1054(1980).  
 RN [5]  
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RX MEDLINE=80001357; PubMed=113060;  
 RA Connell G.E., Parr D.M., Hofmann T.;  
 RT "The amino acid sequences of the three heavy chain constant region  
 domains of a human IgG2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RN [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RX MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Parr D.M.;  
 RT "A note of the amino acid sequence of residues 381-391 of human  
 immunoglobulins gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Parr D.M.;  
 RL Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RX MEDLINE=95255298; PubMed=7737190;  
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 immunoglobulins.";  
 RL Eur. J. Biochem. 228:886-893(1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).  
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 or send an email to license@isb-sib.ch).  
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 CC EMBL: J00230; AAB59393.1; -  
 DR PIR: A02148; G2HU.  
 DR HSSP: P01857; 1FC1.  
 DR TIM: 147110; -  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART: SM00410; Ig\_Like; 1.  
 DR SMART: SM00407; IgC1; 2.  
 DR PROSITE: PS00290; Ig\_MHC; 2.  
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 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83  
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 QY 182 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHCTCPAPELLEG 241  
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 QY 242 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKREOYN 301  
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 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-4 chain C region.

GN IGHG4.  
 OS Homo sapiens (Human).  
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 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83157104; PubMed=6299662;  
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
 RL DNA 1:11-18(1981).  
 RN [2]  
 RP SEQUENCE OF 1-30 AND 81-326.  
 RX MEDLINE=70207560; PubMed=4192699;  
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
 constant region of a gamma 4 chain.";  
 RL Biochem. J. 117:33-47(1970).  
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 CC -----  
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 DR PIR; A02150; G4HU.  
 DR HSP; P01842; 7FAB.  
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 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_like; 1.  
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 DR PROSITE; PS00290; Ig\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 220 CH2.  
 FT DOMAIN 221 327 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
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 FT DISULFID 141 201  
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 QY 182 GLYSLSVVVTPSSSLGTTQYICNVNHNKPSNTKYDKKVPKSCDKTHTCPCPAPPELLGG 241  
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 RESULT 4  
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 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84030930; PubMed=6313520;  
 RA Bernstein K.E., Alexander C.B., Mage R.G.;  
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 F-1 haplotype.";  
 RL Immunogenetics 18:387-397(1983).  
 RN [2]  
 RP SEQUENCE OF 1-128.  
 RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit  
 immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
 heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=70110015; PubMed=5461106;  
 RA Truchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 immunoglobulin G.";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (In) Killander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 RL Stockholm (1967).  
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
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 CC MARKERS, AND REF.5 THE E15 MARKER.  
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 CC -----  
 DR EMBL; M16426; AAA31289.1; -.  
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FT CONFLICT 187 Q -> E (IN REF. 3 AND 5).
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FT CONFLICT 233 E -> Q (IN REF. 5).
FT CONFLICT 246 N -> D (IN REF. 5).
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Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 125 KGPSVFLPAPSSKSTSGCTAALGCLVDPPEPVTVVSWNSGALTSVGHVFPVAVLQSSGLY 184
Db 4 KAPSVFLPAPCGDPTSPSTVTGLCLVKGYPPEPVTVVSWNSGTLTGVRTPFVSQSSGLY 63

QY 185 SLSSVVTVSSSLGQTQYICNVNHPKSNKVKDKKVEPKCDKTHTCPGCPAPPELLGGPSV 244
Db 64 SLSSVVTVSSS--QPVTCTVNAHPATNKVDKTVAPSTCSK---PTCEPPELLGGPSV 116

QY 245 FLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQVNSTY 304
Db 117 FLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQVNSTY 176

QY 305 RVVSVLTVLHQLDNLGKGYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPLPSRDELTK 364
Db 177 RVVSVLTPLTHQDLNGLKGFCKVSNKALPAPIEKTISKARGQPLEKPVYTMGPPREELSS 236

QY 365 NOVSLTCLVKGYPSPDIAVENESNGQPNENYKTPPVLDSDGSEFFLYSKLTVDKSRWQ 424
Db 237 RVSLTCLMINGYPSPDISVEKNGKAEDNYKTPPVLDSDGSEFFLYSKLTVSEWQRG 296

QY 425 NVFSCSVMEALHNNHYTKSLSPGK 451
Db 297 DVFTCSVMHEALHNNHYTKSLSPGK 323

RESULT 5
GC2_GAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_Taxid:10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE-71058471; PubMed-5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
```

```
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE-71058486; PubMed-5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE-75036072; PubMed-4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE-75036073; PubMed-4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE-71058474; PubMed-4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHID 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 50.5%; Score 1216.5; DB 1; Length 329;
Best Local Similarity 70.4%; Pred. No. 6.4e-77;
Matches 235; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 121 SASTKGPSVFLPAPSSKSTSGCTAALGCLVDPPEPVTVVSWNSGALTSVGHVFPVAVLQ 180
Db 1 SARTTAPSVFLPAAACVDTSSMTTGLCLVKGYPPEPVTVVSWNSGALTSVGHVFPVAVLQ- 59

QY 181 SGLYSLSVVTVVPSVSLGQTQYICNVNHPKSNKVKDKKVEPKCDKTH--TCPGCPAPEL 238
Db 60 SGLYSLSVTVVPSVSLGQTQYICNVNHPKSNKVKDKKVEPKCDKTH--TCPGCPAPEL 115

QY 239 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 298
Db 116 LGGPSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 175

QY 299 QYNSTYRVVSVLTVLHQLDNLGKGYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPLPS 358
Db 176 QYNTYRVSVLPIQHQLDNLGKGFCKVSNKALPAPIEKTISKAKGAPRMPDYTLPLPS 235

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGSEFFLYSKLTV 416
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Db 236 RDELSSKSVSTCLINFFPADLHVWASNRVPVSEKEYKNTPPIEDADGSGVFLYSKLTIV 295
QY 417 DKSRRWQGNVFSVSMHEALHNHYTKQSLSPG 450
Db 296 DKSAMDQGTVTCTSVSMHEALHNHYTKQSLSPG 329

RESULT 6
GC3_HUMAN
ID GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT gamma 3 heavy-chain disease protein WIS.";
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RT quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=6808505;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT Structure of the FC fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CHI REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
CC
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CC
CC EMBL; J00231; AA52805.1; ALT_SEQ.
DR PIR; A02149; G3HOW1.
DR HSSP; P01857; 1FC1.
DR MIM; 147120; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT HINGE.
FT CH2.
FT CH3.
FT DOMAIN 74 183
FT DOMAIN 184 289
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
FT VARIANT 139 139
FT VARIANT 182 182
FT VARIANT 227 227
FT VARIANT 227 227
FT VARIANT 279 279
FT SEQUENCE 290 AA; 32331 MW; E69C8C95705B2F46 CRC64;
Query Match 47.9%; Score 1156; DB 1; Length 290;
Best Local Similarity 90.5%; Pred. No. 8.1e-73;
Matches 210; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 220 EPKSCDKTHTCPGCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKF 279
Db 59 EPKSCDTTPPCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVQF 118
QY 280 NNYVDGVVHNAKTPRDEQYNSTYRVVSVLTVLDHQLWLNKGYKCKVSNKALPAPIEKT 339
Db 119 KHYVDGVVHNAKTPRDEQYNSTYRVVSVLTVLDHQLWLNKGYKCKVSNKALPAPIEKT 178
QY 340 ISKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTP 399
Db 179 ISKTGQPREQVYTLPPSRDEMTKNOVSLTCLVKGFPSDIAVEWESGQENNYNTP 238
QY 400 PVLDSGDSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTKQSLSPGK 451
Db 239 PMLDSGDSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTKQSLSPGK 290

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## RESULT 7

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GCL_RAT
ID GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Ig; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45E949B9DA CRC64;

Query Match 47.8%; Score 1152; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 1.8e-72;
Matches 210; Conservative 53; Mismatches 60; Indels 10; Gaps 4;

QY 122 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSWNSGALTSGVHTFPAVLQSS 181
D 1 AETAPSVYPLAPGKDTALGCLVKGYPPEPTVTVNSGALSSGVHTFPAVLQ-S 59
QY 182 GLYSLSVVTVPSSSLTQTYICNVNHPKSNKTKVDKKEPKS-----CDKTHTCPPCPA 241
D 60 GLYLTSSVT--SSTWPSQTVTCNVAHPASSTKVDKKEPKS-----CDKTHTCPPCPA 117
QY 242 ---PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVEVHNAKTPREE 298
D 114 SEVSSVFIFPPKPKDVLITILTPKVTGVVVDISQDDPEVHFSWEDVDVHTAQRPEE 173
QY 299 QYNSTYRVVSVLTVLHODWLNKEYCKKVSNNKALPAPIKTIISKAKGPREQVYTLPPS 358
D 174 QNSTRFRSVELPIHODWLNKEYCKKVSNNKALPAPIKTIISKAKGPREQVYTLPPS 233
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
D 234 KEEMTQNEVSIICVKGYPDIYVEQMNGQPENYKNTPTPTMDTDGSIYFLYSLKLVNK 293
QY 419 SRWQGNVPSVSMHEALHNNHYTKSLSPGK 451
D 294 EKWQGNFTTCSVLHGLHNNHTEKSLSPGK 326
```

## RESULT 8

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GCL_RAT
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
```

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GCL_RAT
ID GCL_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2b chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D40A6 CRC64;

Query Match 47.6%; Score 1146.5; DB 1; Length 333;
Best Local Similarity 64.0%; Pred. No. 4.4e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 9; Gaps 3;

QY 122 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSWNSGALTSGVHTFPAVLQSS 181
D 1 AETAPSVYPLAPGKDTALGCLVKGYPPEPTVTVNSGALSSGVHTFPAVLQ-S 59
QY 182 GLYSLSVVTVPSSSLTQTYICNVNHPKSNKTKVDKKEPKS-----CDKTHTCPPCPA 235
D 60 GLYLTSSVT--SSTWPSQTVTCNVAHPASSTKVDKKEPKS-----CDKTHTCPPCPA 117
QY 236 PELIGSPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVEVHNAKTP 295
D 118 PELIGSPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYDGVVEVHNAKTP 177
QY 296 REEQNSTYRVVSVLTVLHODWLNKEYCKKVSNNKALPAPIKTIISKAKGPREQVYTL 355
D 178 REEQNSTYRVVSVLTVLHODWLNKEYCKKVSNNKALPAPIKTIISKAKGPREQVYTL 237
QY 356 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSDGSFFLYSKLT 415
D 238 GPTTQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPVLDSDGSFFLYSKLT 297
QY 416 VDKSRWQGNVPSVSMHEALHNNHYTKSLSPGK 451
D 298 VERSRWDSRAPVCSVHGLHNNHTEKSLSPGK 333
```

## RESULT 9

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GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
```

DE Ig gamma-1 chain C region.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
RT gamma 1 chain gene";  
RL Cell 18:559-568(1979).  
RN [2]  
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
RX MEDLINE=80202559; PubMed=6769752;  
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
RT cloned in a bacterial plasmid";  
RL Gene 9:87-97(1980).  
RN [3]  
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=80012837; PubMed=113776;  
RA Rogers J., Clarke P., Salser W.;  
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
RT heavy chain";  
RL Nucleic Acids Res. 6:3305-3321(1979).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=78242288; PubMed=98524;  
RA Adetugbo K.;  
RT "Evolution of immunoglobulin subclasses. Primary structure of a  
RT murine myeloma gamma chain";  
RL J. Biol. Chem. 253:6068-6075(1978).  
RN [5]  
RP DISULFIDE BONDS (MOPC 21).  
RX MEDLINE=73008889; PubMed=5073237;  
RA Swasti J., Milstein C.;  
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
RL Biochem. J. 126:837-850(1972).  
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CC -----  
DR EMBL; V00793; CAA24172.1; -;  
DR EMBL; V00793; CAA24173.1; -;  
DR EMBL; V00793; CAA24174.1; -;  
DR EMBL; V00793; CAA24175.1; -;  
DR EMBL; V00795; CAA24176.1; -;  
DR PIR; A02159; GIMS.  
DR HSP; P01842; 7FAB.  
DR GlycoSuiteDB; P01868; -;  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR Pfam; PF00047; Igc1.  
DR SMART; SM00407; Igcl. 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing.  
FT DOMAIN 1 1  
FT NON\_TER 1 97  
FT DOMAIN 98 110 CH1.  
FT DOMAIN 111 217 HINGE.  
FT DOMAIN 218 324 CH2.  
FT DISULFID 27 82 CH3.  
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138 138  
FT CARBOHYD 174 174 N-LINKED (GLCNAC...).  
FT /FTid=CAR\_000055.  
FT DISULFID 244 302  
FT MOD\_RES 324 324 REMOVED POST-TRANSLATIONALLY.  
FT CONFLICT 276 276 N -> D (IN REF. 3).  
FT CONFLICT 278 278 N -> D (IN REF. 3).  
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
Query Match 47.4%; Score 1142; DB 1; Length 324;  
Best Local Similarity 62.0%; Pred. NO. 8.6e-72;  
Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;  
QY 122 ASIKGSPVPLAPSSKSTSGGTAALGCLVQVFPPEPTVTVNSGALTSVGVHTFPVQLSS 181  
Db 1 AKTTPSVPLAPGSAQNSMVTLCGLVGYFFPEPTVTVNSGSLSSGVHTFPVQLSD 60  
QY 182 GLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPP--CPAPELL 239  
Db 61 -LYTLSSVTVPSPPRPSETVTCNVNHNKPSNTKYDKKIVPRDCG----CKPCICTVPEV- 114  
QY 240 GGPVFLFPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGVGVHNAKTKPREEQ 299  
Db 115 --SSVFIFFPKPKDVLTLTPKVTGVVDVSKDDPEVQFSFVDDVEVHTAQTQPREEQ 172  
QY 300 YNTRYRVSVLTVLHODWLNKYEKCKVSNKALPAPTEKTISKAKGQPREPQVYTTLPSSR 359  
Db 173 FNSTERSVSELPIMHQDWLNKEFKCRVNSAFAPIEKTISKTKGRKAPQVYTTIPPK 232  
QY 360 DLTKNQSVLTCVKGFPYSDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKKS 419  
Db 233 EQMAKDKVSLTCMITDFPEDITVEWQNGQPAENYKNTQPIPMNTNGSYFYVSKLVNQS 292  
QY 420 RWOQGVFSCVNHVHEALHNHYTKLSLSPGK 451  
Db 293 NWEAGNTFTCSVLHLEGLHNHHTKLSLSPGK 324  
RESULT 10  
GC3\_MOUSE STANDARD; PRT; 329 AA.  
ID GC3\_MOUSE  
AC P22436;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-3 chain C region, secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
RA Tucker P.W., Blattner F.R.;  
RT "Structural analysis of the murine IgG3 constant region gene";  
RL EMBO J. 3:2041-2046(1984).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
DR PIR; B02156; G3MSC.  
DR HSP; P01857; IFCL.  
DR InterPro; IPR003006; Ig\_MHC.



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DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 47.3%; Score 1141; DB 1; Length 329;
Best Local Similarity 64.0%; Pred. No. 1e-71;
Matches 212; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 123 STKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 182
Db 1 TTAPSVPLVPGCDTSGSVTLGCLVKGYFPEPTVKWNGYALSGVHTFPAVLQSSG 59

QY 183 LKSLSSVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCP--PCPAPELLG 240
Db 60 FYSLSLVTVFSSSTQSTVTCVNAHPASKTELKRIEPR-IPKSTPPGSSCPFGNIIIG 118

QY 241 GRSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREQY 300
Db 119 GFSVFIFFPKPKDALMISLTPEKVKCVVVDVSEDDPDVHVSFWFDNKEVHTAWTPREAQY 178

QY 301 NSTRVSVSLVTLHODWLNGLKYEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 360
Db 179 NSTRVSVSLVTLHODWLNGLKYEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRD 360

QY 361 ELTKNQVSLTCLVKGFYPSDIAVEGSENGQPENNYKTPPVLDSDGFFLYSKLTVDKSR 420
Db 239 QMSKKVSLTCLVNTFFSEALSVWERNGELEDQYKNTPPILDSGTYFLYSLKLVATDTS 298

QY 421 WQQGVFSCSVNHEALHNYTKQSLSPGK 451
Db 299 WLQGEIFTCVVHEALHNYTKQSLSPGK 329

RESULT 11
GCIM_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]

RP InterPro: IPR003597; Ig_c1.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
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CC -----
CC EMBL; V00793; CAA24172.1; -
CC EMBL; V00793; CAA24173.1; -
CC EMBL; V00793; CAA24174.1; -
CC PIR; B02159; G1MSM.
CC HSP; P01842; 7FAB.
CC MGD; MGI:96446; Igh-4.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_c1.
CC Pfam; PF00047; Ig_3.
CC SMART; SM00407; IGc1; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC... ).
FT DISULFID 244 302 POTENTIAL.
FT TRANSMEM 340 357 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICEZ7 CRC64;

Query Match 47.2%; Score 1137; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 2.4e-71;
Matches 205; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

QY 122 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTTPSVVPLAPSSAAQNSMTLGLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD 60

QY 182 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCP--CPAPELL 239
Db 61 -LYTSLSSVTVFSSSPRSETVTCVNAHPASSTKVDKIVPRDCG---CKPCICTVPEV- 114

QY 240 GGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREQ 299
Db 119 GGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREQ 299

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Db 115 --SSVFPPKPDVLTITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTPREEQ 172
QY 300 YNSYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
Db 173 FNSTFRSVSELPIMHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSK 232
QY 360 DELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFYSKLTVDKSK 419
Db 233 EQMAKDKVSLTCTMTDFPEPITVENQWNGQPAENYKNTQPIPMNTNGSYFYVSKLVQKS 292
QY 420 WQOGNVFSCSVNHEALHNHYTQKSLSLSPG 450
Db 293 NWEAGNTFTCSVLHLEGLHNHTTKLSLSPG 323

RESULT 12
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DE 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Konaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC -----
DR EMBL; J00451; BAB59655.1;
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR HSSP; P01857; IFCL1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
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FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 46.9%; Score 1130; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 7.5e-71;
Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 123 STGKSPVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 182
Db 1 TTTAPSVYPLVPGCSDTSGSVTLGCLVKGYFPEPTVKMNYGALSNGVTVSSVLQ-SG 59
QY 183 LYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKVKPEKCDKTHTCP--PCPAPELLG 240
Db 60 FYLSLSLVTPSSTWPSQTVCINVAHPASKTELIRKIEPR-IPKPTPPGSSCPGNTLG 118
QY 241 GPSVFLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 300
Db 119 GPSVFIFPPPKPKDALMISLTPKVCVVVDVSEDDPDVHVSFEVDNKEVHTAWQTPREAQY 178
QY 301 NSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Db 179 NSTFRVVSALPIQHDWMRGKEPKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPTPRE 238
QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFYSKLTVDKSR 420
Db 239 QMSKKKYSLTCLVNTFFSEALSVWEERNGELEDQYKNTTPILDSGDTFLYSKLTVDTS 298
QY 421 WQOGNVFSCSVNHEALHNHYTQKSLSLSP 449
Db 299 WLQGEIFTCSVYVHEALHNHTTKLSLSP 327

RESULT 13
GCAA_MOUSE
ID GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
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RT for the evolution of immunoglobulin structure and function.;
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RN Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL; V00798; CAA24178.1; .
DR PIR; A02152; G2MSA.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 330 330
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.7%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. NO. 1.1e-70;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 122 ASTKGSVFLPAPSSSTSGGTAALGCLVKDYFPEPTVSNHGALTSVHTFPVAVLQSS 181
DB 1 AKTAPSVPLAPVCGDTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPVAVLQSD 60

QY 182 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTFKVDKVEPKSCDKTHTCTCPP--CPAPELI 239
DB 61 -LYTLSSSVVTSTWPSQITCNVAHPASSTKVDKIEPRG-PTIKPCPCCKAPNLL 118

QY 240 GGSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 299
DB 119 GGSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 178

QY 300 YNSTIRVSVTLVHLDWLNKGEYKCKVSNKALPAPIEKTIISKAGQPREPQVYTLPPSR 359
DB 179 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPKSVRAPQVYVLPPE 238

QY 360 DELTKNQVSLTCLVKGYFSDTAWEWSGQPNENYKTTTPVLDSDGSFELYSKLTVDKS 419
DB 239 EEMTKKQVLTTCMTVDFMPEDIVENTNNGKTELKNTKTEPVLDSDGSFYFMSKLRVEKK 298

QY 420 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 299 NWVERNSYSCSVVHEGLNHHHTTKFSRTPGK 330

RESULT 14
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eumalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT Ig2a and Ig2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RC MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC -----
DR EMBL; J00479; .; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FCI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 46.6%; Score 1123.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. NO. 1.7e-70;
Matches 206; Conservative 53; Mismatches 70; Indels 7; Gaps 2;

QY 122 ASTKGSVFLPAPSSSTSGGTAALGCLVKDYFPEPTVSNHGALTSVHTFPVAVLQSS 181
DB 1 AKTAPSVPLPVPVCGDTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPVAVLQSS 59

QY 182 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTFKVDKVEPK-----SCDKTHTCPPEA 235
DB 60 GLYTLSSSVVTSTWPSQITCNVAHPASSTKVDKIEPRVITQNPCHQVPPCAA 119

QY 236 PELLGGSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 295
DB 120 PDLGGSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 179

QY 296 REQYNSTYRVSVTLVHLDWLNKGEYKCKVSNKALPAPIEKTIISKAGQPREPQVYTL 355
DB 180 HREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPRGVAPQVYL 239

QY 356 PPSRDELTKNQVSLTCLVKGYFSDTAWEWSGQPNENYKTTTPVLDSDGSFELYSKLT 415
DB 240 PPAEEMTKKQVLTTCMTVDFMPEDIVENTNNGKTELKNTKTEPVLDSDGSFYFMSKLR 299

QY 416 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

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Qy 62 DSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVSS 121
Db 60 DSVKGRFTYIKDKDRNLSLQMSLSRSEDYAMTCAR-----GDYSAYWGPGLTVTSA 113
Qy 122 ASYKGSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 181
Db 114 AKTTPSVVPLAPGSAQNTSMVTLGCLVKGYFPEPTVTSWNSGSLSGVHTTFAVLQSD 173
Qy 182 GLXSLSSVTVPSSSLGDTYICNVNHNKPSNTKVDKVEPKSCDKTHTCTPP--CPAPEL 239
Db 174 -LVTLSSTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG---CKPCICTVPEV- 227
Qy 240 GGPVSFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNATKKREEQ 299
Db 228 --SSVFIFFPKPKDVLITLTTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREQ 285
Qy 300 YNSTRYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYITPPSR 359
Db 286 FNSTRFSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRKPAQVYITPPPK 345
Qy 360 DELTKNOVSLTCLVKGYFSPDITAVESWGQPENNYKTPPVLDSDGSFELYSLIVDKS 419
Db 346 EQMAKQVSLTCLVITDFFEDITVFWQNGQPAENYKNTQPMIDTDSGYFYSLKLVQKS 405
Qy 420 RWQGNVFCSCVMHEALHNHYTKQSLSPGK 451
Db 406 NWEAGNTFTCSVLHGLHNHHTKELSHSPGK 437

RESULT 2
Q91205 PRELIMINARY; PRT; 473 AA.
ID Q91205
AC Q91205
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.1%; Score 1522.5; DB 11; Length 473;
Best Local Similarity 63.0%; Pred. No. 1.3e-116;
Matches 289; Conservative 64; Mismatches 93; Indels 13; Gaps 5;

Qy 1 OVQLVGGGLVQPGGSLRLSCAASGFTFRSNAGWVRQAPKGLGWVSGISGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAGWVRQAPKGLGWVSGISGGSTYY 79
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVS 119
Db 80 ADTVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVS 135
Qy 120 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQ 179
Db 136 SSARTTPPSVYPLAPGCGDGTSSVTLGCLVKGYFPEPTVTSWNSGSLSSVHTTFAVLQ 195
Qy 180 SSGILSSVTVTPSSSLGDTYICNVNHNKPSNTKVDKVEPKSCDKTHTCTPP----- 232
Db 196 -SGLYTHSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG---CKPCICTVPEV 254
Qy 233 CPAPELLGGGSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNATK 292
Db 255 CPAPNLEGGSPVIFPPNPKIDMLISLTLPKVTCTVVDVSEDDPDVQVLSWFVNNVEHTAQ 314
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Qy 293 TKPREQYNTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQV 352
Db 315 TQTHREDYNTSTRVVSALPIHQDWMSGKEFKCKVNNKDLSPSTRTSKIKGLVRAPOV 374
Qy 353 YTLPPSRDELTKNOVSLTCLVKGYFSPDITAVESWGQPENNYKTPPVLDSDGSFELY 412
Db 375 YILPPPAEQLSRKDVSLTCLVGVFNPGDISVETWNGHTTEENYKDTAPVLDSDGSFY 434
Qy 413 KLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451
Db 435 KLDIKTSKWEKTSDFSCNVSRHEGLKYNLYLKKTISRSPGK 473

RESULT 3
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4
AC Q99LC4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00406; IgV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; Ig_MHC; UNKNOWN.1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 61.5%; Score 1483.5; DB 11; Length 463;
Best Local Similarity 59.6%; Pred. No. 2e-113;
Matches 270; Conservative 78; Mismatches 94; Indels 11; Gaps 5;

Qy 1 OVQLVGGGLVQPGGSLRLSCAASGFTFRSNAGWVRQAPKGLGWVSGISGGSTYY 60
Db 20 OVQLVGGGLVQPGGSLRLSCAASGFTFRSNAGWVRQAPKGLGWVSGISGGSTYY 79
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIIDYWGQGLTVTVS 120
Db 80 SEKFKGKATLTTDKSSSTAYMHLSTLSDSAVYFCARSSYY-YDLPAYWQGLTVTVS 138
Qy 121 SASYKGSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQ 180
Db 139 AAKTTPSVYPLAPGSAQNTSMVTLGCLVKGYFPEPTVTSWNSGSLSGVHTTFAVLQ 198
Qy 181 SGLYSLSSVTVTPSSSLGDTYICNVNHNKPSNTKVDKVEPKSCDKTHTCTPP--CPAPEL 238
Db 199 D-LYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG---CKPCICTVPEV 253
Qy 239 LGSPSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNATKKREE 298
Db 254 ---SSVFIFFPKPKDVLITLTLPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPRE 310
Qy 299 QYNSTRYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQRPFPQVYITPPS 358
Db 311 OFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRKPAQVYITPPP 370
```









RT "NEDO human cDNA sequencing project.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK027379; BAB55072.1; -; 9A1D7AEB5AE4C0E CRC64;  
SQ SEQUENCE 494 AA; 53088 MW; 34.6% Score 834; DB 4; Length 494;

Query Match 34.6%; Score 834; DB 4; Length 494;  
Best Local Similarity 41.8%; Pred. No. 4.2e-60;  
Matches 199; Conservative 62; Mismatches 171; Indels 44; Gaps 16;

```
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGRDIYY 79
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAAYVYCAKHTG--GGVWDPIDYWGQGLTV 119
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 RDSVKGRFTISRDNKNTLYLQMSLRADTAAYVYCARDSCNGAICYCFGWQGLTVTV 139
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 SSASTKGPSVFELPAPSSKSTGGTAAAGCLVKDYFP-EPVTVSNNSGALTSGVHTFP 178
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 SSASPTSPKVPFLSICS--TOPDGNWVIAICLVQGFQEPQLSVTWSESGQGVARNPPSQ 198
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 QSSG-LYLSLSVTVVPSS-LGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCAP 236
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 199 DASGDLKTTSQLTPATQCCLAGKSVTCHVKHY-TNPSQDVTV-----PCPVP 245
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 237 ELLGGPSVFELPPKPK-----DTLMISRTPEVTCVVVDVSHEDPEVKFNW 281
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 246 STPTTPSPST--PTTPSPCHPRLSLRPALEDLLLGSEANLCTLGL-RDASGVTFW 303
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 282 YVDGVEVHNATKPREQYNTYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTIS 341
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 304 TPSSGK--SAVGQPPERLDCGYSSVSLPGCAEPNWHGKTFTCTAAYPESKTPLTATLS 361
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 342 KAKGPREPOVYTLPPSRDELTKNQ-VSLTCLVKGYFSPDAVAVESWNGO--PENNYKTT 398
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 362 KS-GNTFPEVHLLPPSEELALNELVTLCLARGFSPKDVLVRLWLOGSQELPREKTLTW 420
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 399 PPVLD-SDG--SFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 451
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 421 ASRQPSQGTTFVAVTSILRVAEDWKKGDTFSCMGVHGHEALPLAFTQKTTIDRLAG 476
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 11  
Q99KA4 ID Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 52.6 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC004786; AA04786.1; -;  
DR HSSP: P01810; 25BJ  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003597; Ig\_cl.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig\_4.  
DR SMART: SM00409; IG; 3.  
DR SMART: SM00407; IGcl; 3.  
DR SMART: SM00406; IG; 1.  
DR SMART: SM00410; IG\_like; 1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

```
Query Match 34.0%; Score 820.5; DB 11; Length 487;  
Best Local Similarity 40.4%; Pred. No. 5.3e-59;  
Matches 188; Conservative 78; Mismatches 170; Indels 29; Gaps 15;  
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 20 EVOLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVATISDGGSTYY 79  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAAYVYCAKHTG--GVWDPIDYWGQGLTV 117  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 80 PDNVKGRFTISRDNKNTLYLQMSLRADTAAYVYCARDMGSPYGGYSRFDYWGQGTI 139  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 118 TVSSASTKGPSVFELPAPSSKSTGGTAAAGCLVKDYFPE-PVTVSNNSGALTSGVHTFPA 176  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 140 TVSSASARNPTIYPLT-LPRALSSDPVIGLCLHDYFPSTGNVTWTKSGKDIITVTFPP 198  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 177 VLOSSGLYSLSSVTVVPSSSLGT-QTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPA 235  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 199 ALASGGYTMSSQLTLPAVECEGESVKCSVQH--DSNAVQELDVKCGPPPPCP- 254  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 236 PELLGGPSVFELPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNHYDGVVHNAKTKP 295  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 255 PSC--HPSLSLORPALED-LLLGSDASLFTCLTNGLRNPEGAV-FTW----EPSTGKDAV 305  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 296 REBOYNST---YRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQV 352  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 306 QKAVQNSCGCYSSVSLPGCAERNWSGAFKCTVTHPESDT-LGTIAKITVTFPPQV 364  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 353 YTLPPSRDELTKNQ-VSLTCLVKGYFSPDAVAVESWNGO---PENNYKTPPVLDSDG-- 406  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 365 HLLPPSEELALNELVTLCLRAFNPKEVLVRLHNGEELSPESLYLPEPLKEPGE 424  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 407 SFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 451  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 425 TYLVTSVLRSVSAETWKGQDYQSCMGVHGHEALPMNFTQKTTIDRLSGK 469  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  


```

RESULT 12  
Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.  
AC Q91WP5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 51.6 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013656; AA013656.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 32.3%; Score 778.5; DB 11; Length 479;  
Best Local Similarity 39.5%; Pred. No. 1.4e-55;  
Matches 183; Conservative 80; Mismatches 167; Indels 33; Gaps 16;

```
QY 1 QVOLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 20 EVOLVESGGGLVQPGGSLRVSCAASGLTFSNYAMSVVRSPEKRLWVAAINSGNTYY 79  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAAYVYCAKHTGGGVWDPIDYWGQGLTVTVS 120  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 80 SDTMKGRFTISRDNKNTLYLQMSLRADTAAYVYCAKHTGGGVWDPIDYWGQGLTVTVS 133  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 121 SASTKGPSVFELPAPSSKSTGGTAAAGCLVKDYFPE-PVTVSNNSGALTSGVHTFPVLIQ 179  
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  


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Db 134 SEPAEPTIYPLT-FPOALSSDPVIGLIIHDFPSCGMNVTWKGSKGDIITVNEPPALA 192

QY 180 SSGLYSLSSVTVTPSSSLGT-OTVICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238

Db 193 SGGRYTSSQTLPAVCPGESVKCSQVH-DSNPVQELNVNCPGICSPPTTPPPSCQ- 250

QY 239 LGGPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPE-VKFNWYVDGVVHNAKTPRE 297

Db 251 --FSLSLORPALED-LLIGSDASITCLNGL--RDEGAVFTW----EPSTGKDAVQK 299

QY 298 EOYNST---YRVSVLTVLHODWLNKGYCKKVSNNKALPAPIEKTISKAKGQPREQVYTT 354

Db 300 KAVQNSCGCYSVSVLPGCAERWNSGASFCKTHTHPESDT-LGTIAKVTVNTFPQVHL 358

QY 355 LPPSRDELTKNO-VSLCLVKGFVPSDIAVWESNGQ---PENNYKTTTPVLDSDG--SF 408

Db 359 IPPPSEELALNELVSLTCLVRAFNPKVLRVWLHNGNEELSPESYLVEPLKEPGEGATTY 418

QY 409 FLYSKLTVDKSRWQOOGVNFSCVMHEALHNHYTKQSLSPGK 451

Db 419 LVTSLVLRVAEINKQDQYSCMVGHEALPMNFTQKTIIDRLSGK 461

RESULT 13

Q96GA6 PRELIMINARY; PRT; 614 AA.

AC Q96GA6

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE UNKNOWN (PROTEIN FOR MGC:15420).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PRIMARY B-CELLS FROM TONSILS;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC009851; AAH09851.1; --

SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 31.9%; Score 768.5; DB 4; Length 614;

Best Local Similarity 31.8%; Pred. No. 1.3e-54;

Matches 177; Conservative 90; Mismatches 178; Indels 111; Gaps 15;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

Db 20 QMQLVQSGAEVKKTKSSVKYSCKASGYTFYRLHWVRQAPGQALEWMMGWITPFGNTNY 79

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVDPIDYWGQTLVTS 120

Db 80 AQRFQDRTVITRDSEMTATWELSSLRSEDTAMYCARGYSSWDADFQWGGTQWTVS 139

QY 121 SASATGSPVFLPAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSVHTFPV 177

Db 140 SGSASAPTLPLVSCENSPSDTSSVAVGCLAQDFLPSDITFSWKYKNNDSISSTRGFPV 199

QY 178 LQSSGLYSLSSVTVTPSSSL-GTQIY-ICNVNHNKPSN-----TKVDKKE 220

Db 200 LR-GGKYAATSQVLLPSKDMOGTDEHVCKVQHPNGNEKKNVPLPVIAPLPPKVSFVFP 258

QY 221 PKS-----CDKTHCTP-----PCPAPELLGSPS---- 243

Db 259 PRDFFGNPKSKLICQATGFSRQIQVSWLRGKQVGGVTTDQVQAKESGPTTYKV 318

QY 244 -----VFLEPPPKDKTLMIS 258

Db 319 TSTLTIKESDWLSQSMFTCRVDRHGLTFQQAASSMCMVDPQDQTAIRFAIPPS-FASIELT 377

QY 259 RTPVTCVVDVSHEDPEVFNWYVDGVVHNAKTKPREQYNSTYRVSVLTVLHODWLN 318

Db 259 RTPEVTCVVDVSHEDPEVFNWYVDGVVHNAKTKPREQYNSTYRVSVLTVLHODWLN 318

Db 259 RTPEVTCVVDVSHEDPEVFNWYVDGVVHNAKTKPREQYNSTYRVSVLTVLHODWLN 318

Db 378 KSKLTCLTCLTDLTTVD-SVTISWTRQNGRAVKTHTNISESHNPATFSAVGEASICECDWN 436

QY 319 NOKEYKCKVSNKALPAPIEKTISKAKGQ-REPQVYTLPPSRDELT-KNOVSLTCLVKGP 376

Db 437 SGERETCTVTHTDLSPLKQTSRPRKVALHRPDVLYLLPAPREQLNRESATITCLVTGF 496

QY 377 YPSDLAVENESGQ-ENNYYKTTTPVLD--SDGSFFELYSKLTVDKSRWQOOGVNFSCVM 432

Db 497 STADVFVQMQGQPLSPKPYTSAPMPPEQAPGRYFAHSILTVSEEWNTGETITCYVA 556

QY 433 HEALHNHYTKQSLSPGK 448

Db 557 HEALPNRVTVTVDKS 572

RESULT 14.

Q91Z07 PRELIMINARY; PRT; 486 AA.

AC Q91Z07

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE HYPOTHETICAL 52.7 KDA PROTEIN.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC010324; AAH10324.1; --

KW Hypothetical protein.

SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 31.8%; Score 766; DB 11; Length 486;

Best Local Similarity 38.2%; Pred. No. 1.5e-54;

Matches 179; Conservative 84; Mismatches 169; Indels 36; Gaps 17;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60

Db 20 EYHLVESGGGLVKPGGSLKSLSCVSGFSTSYDMSWVRQTPERRLEWAAIT-SGGNTYY 78

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAK-----HTGGGVDPIDYWGQ 114

Db 79 PNWVGRFTVSRDNKNTLYLQMNLSKSEDTAMYICVPRPEIPIYYSYFDS---WGQG 135

QY 115 TLTVYSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPE-PVTVSNWSGALTSVHT 173

Db 136 TTVTVSSSARNTIYPLT-LPRALSSDPVIGLIIHDFPSCGMNVTWKGSKGDIITVN 194

QY 174 FPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCP 232

Db 195 FPAALASGGGYTSSQLTLPAVECPGESVKCSQVQH---DSNAVQELDKVCSGPPPPCP 251

QY 233 CPAPPELLGSPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAK 292

Db 252 CP-PSC--HPSLSIORPALED-LLIGSDASITCLNGLNRPAGV-FTW----EPSTGK 301

QY 293 TKPREQYNST---YRVSVLTVLHODWLNKGYCKKVSNNKALPAPIEKTISKAKGQPRE 349

Db 302 DAVQKKAQVNSCGCYSVSVLPGCAERWNSGASFCKTHTHPESDT-LGTIAKVTVNTFP 360

QY 350 PQVYTLPPSRDELTKNQ-VSLTCLVKGFVPSDIAVWESNGQ---PENNYKTTTPVLDSD 405

Db 361 POVHLPPPSEELALNELVSLTCLVRAFNPKVLRVWLHNGNEELSPESYLVEPLKEPGE 420

QY 406 G--SEFFLYSKLTVDKSRWQOOGVNFSCVMHEALHNHYTKQSLSPGK 451

Db 421 GATTILTVSLVRSATETWKGQDQYSCMVGHEALPMNFTQKTIIDRLSGK 468

RESULT 15

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Q91XE1
ID Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:4224494) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010798; AAH10798.1; -.
FT NON_TER 1
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 31.3%; Score 755.5; DB 11; Length 480;
Best Local Similarity 39.6%; Pred. No. 1.1e-53;
Matches 183; Conservative 73; Mismatches 175; Indels 31; Gaps 16;

QY 2 VQLVQSGGLVQPGSLRLSCAASGTFTRSNAMGWVRQAPGKLEWVSGISGGSTYYA 61
Db 20 VKLVEGGGLVKPGSLRLSCAASGTFISNSYMSWVRQTPKRLWVATISNGYATHYP 79
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGOGTLTVSS 121
Db 80 DSMKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGOGTLTVSS 135
QY 122 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYPE-PVTVSWNSGALTSGVHTFPAVLQS 180
Db 136 EPAREPTIYPLT-PPQALSDPVIIGCLIHDPFSGTMVNTGKSGKIDITVNFPPALAS 194
QY 181 SGLYSLSSVTVFSSSLGT-OTYICNVNHPKSNKYDKVKKPKSCDKTHTCPCPAPELL 239
Db 195 GGRTYMSQLTLPAVEGEGESYKCSVQH-DSNPVQELNVNCPGICSPPTTPPPSCQ-- 251
QY 240 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPE-VKFNMYVDGVEVHNAKTPREE 298
Db 252 --PSLSLQRPALSD-LLLSGDSAITCTLNGL--RDPEGAVFTW-----EPSTCKDAVQKK 301
QY 299 QYNST---YRVSVLVTLVHODMLNGKEYCKKVSNNKALPAPIEKTIISKAKGQPREPQVYTL 355
Db 302 AVQNSCGCYSVSVLPGCAERNWSGASFKCTVTHPESDT-LTGTIAKVTNTVPPQVHLL 360
QY 356 PPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTPPPVLDSDG--SFF 409
Db 361 PPFSEELALNELLSLTCLVRAFNPKVLRVHLHGNEELSPESYLVEPLKEPGEGATYTL 420
QY 410 LYSKLTVDKSRWQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 451
Db 421 VTSVLRVSAEINWKGQDQYSCWNGHEALPMNFTKIDRLSGK 462
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Search completed: October 9, 2002, 19:12:26  
Job time : 39.5421 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:05:30 ; Search time 18.801 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 1146  
Sequence: 1 EIVLTQSLPLVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaea.\*

ALIGNMENTS

RESULT 1

Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.  
AC Q99M37;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HYPOTHETICAL 26.3 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS  
RC TISSUE.;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002035; AA02035.1; -.  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_LHC.  
DR InterPro; IPR003596; Ig\_LV.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR SMART; SM00410; IG like; 1.  
DR PROSITE; PS00290; IG\_LHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 69.4%; Score 795.5; DB 11; Length 238;  
Best Local Similarity 67.7%; Pred No. 1e-67;  
Matches 149; Conservative 31; Mismatches 39; Indels 1; Gaps 1;  
QY 1 EIVLTQSLPLVTPGEPASISCRSSQSLHLSNGYTYLDWYLPKPGQSPQLLYSGSHRA 60

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	795.5	69.4	238 11 Q99M37	Q99M37 mus musculus
2	635	55.4	214 11 Q9RIA5	Q9RIA5 mus musculus
3	628	54.8	211 11 Q9IXL0	Q9IXL0 mus musculus
4	624.5	54.5	235 11 Q9IWL2	Q9IWL2 mus musculus
5	621	54.2	234 11 Q9IWF8	Q9IWF8 mus musculus
6	609	53.1	233 11 Q9IWS9	Q9IWS9 mus musculus
7	428.5	37.4	114 4 Q9UL80	Q9UL80 homo sapien
8	407	35.5	236 4 Q96E61	Q96E61 homo sapien
9	406	35.4	104 11 Q9JL82	Q9JL82 mus musculus
10	376.5	32.9	235 11 Q99M11	Q99M11 mus musculus
11	373	32.5	109 4 Q9UL78	Q9UL78 homo sapien
12	370.5	32.3	233 11 Q9IV32	Q9IV32 m adult mal
13	369	32.2	109 4 Q9UL86	Q9UL86 homo sapien
14	364.5	31.8	233 4 Q96I69	Q96I69 homo sapien
15	351.5	30.7	108 4 Q9UL83	Q9UL83 homo sapien
16	340.5	29.7	111 11 Q920E9	Q920E9 mus musculus

Db	20	DVMTQPLSLPVLGDOASISCRSSQSIHNSGNTYLEWYLOKPGQSKLLIYKVSRRF	79
Qy	61	SGVPDRFSGSGVTGDTFLRISRVEADGVGYCMQGLQSPFTFGPTKVDIKRGTVAAAPS	120
Db	80	SGVPDRFSGSGVTGDTFLRISRVEADGLGVYCFQGSHPYTFGSGTKLEIKRAD-AAPT	138
Qy	121	VFIFPPSDQLKSGTASVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	180
Db	139	VSIFPPSSEQLTSGGASVCFVFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDSKDSSTYS	198
Qy	181	LSSTLTLSKADYKHKYKACEVTHOGLSSPVTKSFNRGEC	220
Db	199	MSSTLTLTDEYERHNSYTCEATHKTKSTSPVKSFRNEC	238
RESULT 2			
Q9RIA5	PRELIMINARY;	PRT;	214 AA.
AC	Q9RIA5;		
DT	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DE	KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	SEQUENCE FROM N.A.		
RA	Wildie K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;		
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a		
RT	submitted antibody (scFv).";		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF152371; AAB04242.1; -		
DR	HSSP; P01679; 2FBJ.		
DR	InterPro; IPR003600; Ig-like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Profam; PF00047; Ig; 2.		
DR	SMART; SM00406; Igv; 1.		
DR	SMART; SM00410; Ig_Like; 1.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		
FT	NON_TER	1	
FT	NON_TER	214	
SQ	SEQUENCE	214 AA; 23922 MW; 52BA205FDE995E2A CRC64;	
Query Match			
Best Local Similarity			
Matches 121; Conservative 37; Mismatches 56; Indels 6; Gaps 2;			
Qy	1	EIVLTQSPLSPLPVTGEPASISCRSSQSLHNSGYTYLDWLQKPGQSPOLLIVSGSHRA	60
Db	1	DIQLTQSPSPMTASIGERVITICRASQDI-----NSYLSWFQQRPGSKPTLIYRANRLV	55
Qy	61	SGVPDRFSGSGVTGDTFLRISRVEADGVGYCMQGLQSPFTFGPTKVDIKRGTVAAAPS	120
Db	56	DGVPSRFSGSGSQDYSLTISLSEYEDMGVYCLQYDEFPFTFGSGTKLEIKRAD-AAPT	114
Qy	121	VFIFPPSDQLKSGTASVCLLNNFYPRAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS	180
Db	115	VSIFPPSSEQLTSGGASVCFVFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDSKDSSTYS	174
Qy	181	LSSTLTLSKADYKHKYKACEVTHOGLSSPVTKSFNRGEC	220
Db	175	MSSTLTLTDEYERHNSYTCEATHKTKSTSPVKSFRNEC	214
RESULT 3			
Q9IXLO	PRELIMINARY;	PRT;	211 AA.
ID	Q9IXLO		
AC	Q9IXLO;		









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Query Match      32.3%; Score 370.5; DB 11; Length 233;
Best Local Similarity 38.3%; Pred. No. 2.7e-27;
Matches 85; Conservative 42; Mismatches 84; Indels 11; Gaps 6;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
DB 20 QAVVTOES-ALTTSPGETVTLTCSRSTGAVTTSNYA--NMVQKPDHFLTGLIGGTTNRA 76
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPGKVDIKRGTVAAPS 120
DB 77 PGVPAREFSGSLIGDRAALTITCAQTEDEAIFYCALWYSS-WVFGGCTKLVLGQPKSSPS 135
QY 121 VFIPTSPDQLKSGTASVCLLNNEYPREAKVQWKVDNALQSGNSQSVTEQDSKST-- 178
DB 136 VTLPSPSELETKATLVCTITDFYGVGVVDWVKVDG--TPVTQGMETQPSKOSNNK 192
QY 179 YLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220
DB 193 YMASSTLTLTARAWERHSSYSQVTHG--HTVEKSLSRADC 232

RESULT 13
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
AC Q9UL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1;
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 109
FT SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match      32.2%; Score 369; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 1.3e-27;
Matches 76; Conservative 11; Mismatches 22; Indels 4; Gaps 1;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGAPRLIYGTSSRA 56
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPGKVDIKR 113
DB 57 TGIPDRFSGSGSETDFTLTISRLEPEDFAVYVQYQYQYSSIFTFGPGKVDIKR 109

RESULT 14
Q96169 PRELIMINARY; PRT; 233 AA.
ID Q96169
AC Q96169;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:12849).
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007782; AAH07782.1;
SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match      31.8%; Score 364.5; DB 4; Length 233;
Best Local Similarity 36.7%; Pred. No. 9.9e-27;
Matches 81; Conservative 44; Mismatches 83; Indels 13; Gaps 6;

QY 3 VLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRASG 62
DB 22 VLTQ-PASVSVAPGQTARITCGS-----NLGSKSVNMYQLRPGAPILVYVENKERPA 75
QY 63 VPDRFSGSVSGTDFTLRISRVEAEDVGYYCM--OGLQSPFTFGPGKVDIKRGTVAAPS 120
DB 76 IPERLSALTSEETATLTISVAVGDEADYFCQVWDTTQQYVFGTGTQTVLQPKRANPT 135
QY 121 VFIPTSPDQLKSGTASVCLLNNEYPREAKVQWKVDNA--LQSGNSQSVTEQDSKSTY 179
DB 136 VTLPSPSELETKATLVCLISDFYPGAVTVAKADGSPVKAG--VETTKPSKSNKY 193
QY 180 SLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220
DB 194 AASSYLSLTPEQWKSHRSYSQVTHG--STVEKTVAPTEC 232

RESULT 15
Q9UL83 PRELIMINARY; PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1;
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108
FT SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match      30.7%; Score 351.5; DB 4; Length 108;
Best Local Similarity 63.7%; Pred. No. 6.1e-26;
Matches 72; Conservative 14; Mismatches 22; Indels 5; Gaps 2;

QY 1 EIVLTQSPVSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
DB 1 EIVMTQSPATLSVSPGERATLSCRASQS-VSSN----LAWYQKPGQAPRLIYCASTRA 55
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPGKVDIKR 113
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Db 56 TGIPARESGSGCTEFTLTITSSLOFEDEFAVYICQHYNNWPFTEGPGTKYDIKR 108

Search completed: October 9, 2002, 19:12:25  
Job time : 19.801 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:12:30 ; Search time 23.5714 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLVPTGPAS.....EVTHQGLSSPVTKSFNRGFC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	220	AAE12714	Human recombinant
2	114	51.8	381	AAE12707	Human biyPHI-IL-2
3	113	51.4	113	AAE12705	Human PH1 Fab anti
4	110	50.0	236	AAV56286	HCAT1 clone 25 anti
5	107	48.6	107	AAE62265	Light chain constr
6	107	48.6	108	AAW06002	Amino acid sequenc
7	107	48.6	108	AAV92191	Human IgG1 kappa d
8	107	48.6	234	AAAS2951	Human anti-IgE Mab
9	107	48.6	468	AAV92196	Human IL-6R-alpha-
10	107	48.6	727	AAV92192	Human gp130-kappa
11	106	48.2	106	AAV81028	C region of L chai

12	106	48.2	106	14	AAE1687	Undefined ORF1 enc
13	106	48.2	106	14	AAE43686	Human kappa consta
14	106	48.2	106	18	AAW37347	Immunoglobulin C-k
15	106	48.2	106	19	AAW59622	Anti-RSV F protein
16	106	48.2	106	19	AAW48649	Constant region of
17	106	48.2	106	22	AAW04072	Interleukin recept
18	106	48.2	107	19	AAW40578	Human kappa CL dom
19	106	48.2	107	20	AAV50152	Human kappa light
20	106	48.2	107	20	AAV08745	Human kappa-CL dom
21	106	48.2	107	20	AAW92425	Human kappa protei
22	106	48.2	107	21	AAE27000	Human kappa CL dom
23	106	48.2	143	10	AAV93559	Sequence of human
24	106	48.2	193	22	AAE52145	Humanised HMFGL 11
25	106	48.2	201	20	AAV29770	P-selectin ligand
26	106	48.2	213	17	AAW04301	Antibody fusion pr
27	106	48.2	213	17	AAW05830	Humanised M291 ant
28	106	48.2	213	22	AAE10510	Humanised high pot
29	106	48.2	213	22	AAE10512	Humanised high pot
30	106	48.2	213	22	AAE10514	Humanised high pot
31	106	48.2	213	22	AAE10516	Humanised high pot
32	106	48.2	213	22	AAE10518	Humanised high pot
33	106	48.2	213	22	AAE10520	Humanised high pot
34	106	48.2	213	22	AAE10522	Humanised high pot
35	106	48.2	213	22	AAE10524	Humanised high pot
36	106	48.2	213	22	AAE10526	Humanised high pot
37	106	48.2	213	22	AAE83157	Humanised high pot
38	106	48.2	214	14	AAE30776	Ganglioside GM2 an
39	106	48.2	214	14	AAE43338	H52L6-158 murine a
40	106	48.2	214	17	AAW05828	Completely humanis
41	106	48.2	214	18	AAW45517	Humanised 1D10 ant
42	106	48.2	214	18	AAW34504	NANUC-2 light chai
43	106	48.2	214	18	AAW34506	Light chain of hum
44	106	48.2	214	18	AAW07615	Ulcerative colitis
45	106	48.2	214	19	AAW64671	Human UC PANCA mon

## ALIGNMENTS

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RESULT 1
AAE12714
ID AAE12714 standard; Protein; 220 AA.
XX
AC AAE12714;
XX
DT 04-JAN-2002 (first entry)
XX
DE Human recombinant immunoglobulin (Ig) light chain region.
XX
KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
KW light chain region; cancer; breast; ovary; lung; bladder;
KW cytostatic; therapy; immunoglobulin; Ig.
XX
OS Homo sapiens.
XX
PN WO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MPG;
XX
DR WPI; 2001-626437/72.
XX
N-PSDB; AAD20744.
XX
PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1 -

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XX PS Claim 12; Page 103; 126pp; English.
XX CC
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human recombinant immunoglobulin
XX CC (Ig) light chain region (variable VL and CL constant kappa light chain).
XX SQ Sequence 220 AA;
Query Match 100.0%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-197;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKRGTVAAAPS 120
DB 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKRGTVAAAPS 120
QY 121 VFIFPPSDEQLKSGTASVYVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
DB 121 VFIFPPSDEQLKSGTASVYVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
QY 181 LSSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 220
DB 181 LSSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 220
RESULT 2
AAE12707
ID AAE12707 standard; Protein; 381 AA.
XX AC AAE12707;
XX DT 04-JAN-2002 (first entry)
XX DE Human bivPH1-IL-2 immunocytokine protein.
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX OS Homo sapiens.
XX PN WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR 30-MAR-2000; 2000US-0538913.
XX PA (DYAX-) DYAX CORP.
XX PI Hoogenboom HRJM, Henderikx MPG;
XX DR *WPI: 2001-626437/72.
XX DR N-PSDB; AAD20732.

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XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1 -
XX PS Claim 9; Page 95-97; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human bivPH1-IL-2
XX CC immunocytokine protein. bivPH1 is mucin specific binding portion.
XX SQ Sequence 381 AA;
Query Match 51.8%; Score 114; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.1e-98;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 186
QY 61 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKRG 114
DB 187 SGVPDRFSGSVSGTDTFLRISRVEAEDGVYYCMQGLQSPFTFGPTGKVDIKRG 240
RESULT 3
AAE12705
ID AAE12705 standard; Protein; 113 AA.
XX AC AAE12705;
XX DT 04-JAN-2002 (first entry)
XX DE Human PH1 Fab antibody variable light chain region (VL).
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
XX KW variable light chain region; cancer; breast; ovary; lung; bladder;
XX KW cytostatic; therapy; PH1 antibody.
XX OS Homo sapiens.
XX PN WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR
XX PA
XX PI
XX DR
XX DR

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PR 30-MAR-2000; 2000US-0538913.  
 PA (DYAX-) DYAX CORP.  
 XX  
 XX  
 PI Hoogenboom HRJM, Henderikx MPG;  
 XX  
 XX WPI; 2001-626437/72.  
 DR N-PSDB; AAD20730.  
 XX  
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member  
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
 PT its portion for binding to an epitope of the protein core of mucin-1 -  
 XX  
 XX Claim 3; Page 93; 126pp; English.  
 XX  
 XX The invention relates to an isolated tumour-associated antigen mucin-1  
 CC (MUC-1)-specific binding member comprising an antigen binding domain  
 CC region having an antibody variable light (VL) or heavy (VH) region,  
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific  
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma  
 CC The binding of MUC1-specific binding member to MUC1 is detected by a  
 CC detection method selected from enzyme-linked immunosorbent assay,  
 CC magnetic resonance imaging, scintillation counting, and x-ray film.  
 CC MUC1-specific binding member is useful for treating cancer, preferably  
 CC adenocarcinoma, in an individual, where the cancer is present in tissue  
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific  
 CC binding member is useful for diagnosing and imaging MUC1-expressing  
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,  
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-  
 CC containing molecules, and for therapeutically or prophylactically  
 CC treating cancer. The present sequence is anti-MUC1 human PhI Fab  
 CC antibody VL region.  
 XX  
 XX Sequence 113 AA;  
 SQ  
 Query Match 51.4%; Score 113; DB 22; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-98;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIVLTQSLPLVTPGEPASISCRSSQLHNSGYTLWDYLQKPGQSPQLLIYSGSHRA 60  
 DB 1 EIVLTQSLPLVTPGEPASISCRSSQLHNSGYTLWDYLQKPGQSPQLLIYSGSHRA 60  
 QY 61 SGVPDRFSGVSGTDTLRLISRVAEADVGYVCMQGLQSPFTFGPTKVDIKR 113  
 DB 61 SGVPDRFSGVSGTDTLRLISRVAEADVGYVCMQGLQSPFTFGPTKVDIKR 113  
 RESULT 4  
 AAY56286  
 ID AAY56286 standard; Protein; 236 AA.  
 XX  
 XX AAY56286;  
 XX  
 XX 08-FEB-2000 (first entry)  
 XX  
 XX HCAT1 clone 25 antibody variable light chain protein sequence.  
 DE  
 XX Human cationic amino acid transporter; hCAT1; targeted delivery;  
 KW gene delivery; virus-like particle; retroviral envelope molecule;  
 KW infection; gene therapy; restenosis; balloon angioplasty;  
 KW smooth muscle cell; transduction.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX EP959136-A1.  
 XX  
 XX 24-NOV-1999.  
 PD  
 XX 20-MAY-1998; 98EP-0201693.  
 PF  
 XX  
 XX 20-MAY-1998; 98EP-0201693.  
 PR

XX (INTR-) INTROGENE BV.  
 PA  
 XX WPI; 2000-001283/01.  
 DR N-PSDB; AA238770.  
 XX  
 XX New virus-like particle or gene delivery vehicle, useful for gene  
 PT therapy -  
 PT  
 XX Claim 13; Fig 16; 66pp; English.  
 PS  
 XX The present invention describes a virus-like particle or gene delivery  
 CC vehicle comprising a ligand capable of binding to a human amino acid  
 CC transporter. The method is useful for the target delivery of substances  
 CC to cells e.g. gene therapy. A human cationic amino acid transporter  
 CC (hCAT1) targeted adenovirus is useful for local applications of  
 CC adenoviral vector e.g. in patients with restenosis following balloon  
 CC angioplasty where smooth muscle cells need to be transduced with an  
 CC adenoviral vector carrying the cENOS cDNA. More efficient transduction  
 CC of tissues can be carried out therefore resulting in lower  
 CC multiplicity's of infections that can be used and therefore less vector  
 CC associated toxicity to the tissues surrounding the target cells. AA238737  
 CC to AA238770, and AAY56264 to AAY56287 represent sequences used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 236 AA;  
 SQ  
 Query Match 50.0%; Score 110; DB 21; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-94;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 111 IRKGTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV 170  
 DB 127 IRKGTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV 186  
 QY 171 EODSKDSTYLSLSTLTSLKADYEHKVKVACEVTHOGLSSPVTKSFNRGEC 220  
 DB 187 EODSKDSTYLSLSTLTSLKADYEHKVKVACEVTHOGLSSPVTKSFNRGEC 236  
 RESULT 5  
 AAB62265  
 ID AAB62265 standard; Protein; 107 AA.  
 XX  
 XX AAB62265;  
 XX  
 XX 11-JUN-2001 (first entry)  
 DT  
 XX Light chain construct 431A amino acid fragment.  
 DE  
 XX Fusion protein; cell surface antigen; cancer; monoclonal antibody;  
 KW light chain construct; carcinoembryonic.  
 KW  
 XX Mammalia.  
 OS  
 XX  
 XX WC200119842-A1.  
 PN  
 XX 22-MAR-2001.  
 PD  
 XX 18-SEP-2000; 2000WO-US25558.  
 PF  
 XX 17-SEP-1999; 99US-0399079.  
 PR  
 XX (GENZ ) GENZYME TRANSGENICS CORP.  
 PA  
 XX Pollock D, Meade HM, Bosslet K;  
 PI  
 XX WPI; 2001-257871/26.  
 DR N-PSDB; AAF57571.  
 DR  
 XX New fusion protein, useful for killing diseased cells e.g. cancer  
 PT cells, comprises fused first and second units, such that the protein  
 PT assembles into complex which optimizes activity of multimeric form of

PT second unit -  
XX  
PS Example 1; Fig 1B; 88pp; English.  
XX  
CC The invention relates to a fusion protein (I) comprising a first member  
CC fused to a second member, where the first and second members are chosen  
CC such that (I) assembles into a complex having a number of subunits which  
CC optimizes activity of the multimeric form of the second member. (I) is  
CC useful for selectively killing an aberrant or diseased cell which  
CC expresses a target antigen on its surface, e.g., a cancer cell expressing  
CC a cell surface antigen. (I) is also useful for detecting in vitro or in  
CC vivo the presence of target antigen in a sample, e.g., for diagnosing a  
CC disease, by contacting a sample or a control sample that allows  
CC interaction of (I) which is labeled, and detecting formation of a  
CC complex. (I) is also useful for selectively directing (e.g., localizing)  
CC the second unit of (I) to the vicinity of an undesirable cell. The  
CC present sequence represents a fragment of a light chain construct 431A  
CC that was generated using the light chain sequence from a humanised Mab  
CC against carcinoembryonic antigen (431).  
XX  
SQ Sequence 107 AA;  
Query Match 48.6%; Score 107; DB 22; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.4e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 173  
DB 1 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 174 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
RESULT 6  
AAW70802  
ID AAW70802 standard; protein; 108 AA.  
XX  
AC AAW70802;  
XX  
DT 03-FEB-1999 (first entry)  
DE Amino acid sequence of the kappa domain.  
XX  
KW gp130; cytokine antagonist; interleukin; gamma-interferon;  
KW granulocyte macrophage colony-stimulating factor; J peptide;  
KW transforming growth factor-beta.  
XX  
OS Synthetic.  
XX  
PN US5844099-A.  
XX  
PD 01-DEC-1998.  
XX  
PF 27-NOV-1995; 95US-0563105.  
XX  
PR 27-NOV-1995; 95US-0563105.  
PR 20-OCT-1993; 93US-0140222.  
XX  
PA (REGE-) REGENERON PHARM INC.  
XX  
PI Economides A, Stahl N, Yancopoulos GD;  
XX  
DR WPI; 1999-044669/04.  
XX  
PT Cytokine antagonists - comprising extracellular domains of  
PT specificity-determining and signal-transducing components of  
PT cytokine receptor  
XX  
PS \*Example, 4; Fig 13; 46pp; English.  
XX  
CC The present sequence represents the amino acid sequence of

CC kappa domain. The protein is used in the course of the invention.  
CC The specification describes cytokine antagonists comprising only the  
CC extracellular domain of the specificity-determining component of  
CC the cytokine receptor and the extracellular domain of a  
CC signal-transducing component of the cytokine receptor. The cytokine  
CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),  
CC granulocyte macrophage colony-stimulating factor (GM-CSF),  
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The  
CC antagonist is capable of binding the cytokine to form a nonfunctional  
CC complex. The compounds have therapeutic activity as cytokine antagonists  
CC and can also be used in assays for identifying novel agonists and  
CC antagonists of cytokines.  
XX  
SQ Sequence 108 AA;  
Query Match 48.6%; Score 107; DB 20; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.5e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 173  
DB 2 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61  
QY 174 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 108  
RESULT 7  
AA92191  
ID AAY92191 standard; protein; 108 AA.  
XX  
AC AAY92191;  
XX  
DT 01-AUG-2000 (first entry)  
DE Human IgG1 kappa domain.  
XX  
KW gp130-C-gamma-1; cytokine; antagonist; CNFP; receptor; fusion protein;  
KW cytostatic; immunomodulator; osteopathic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..2  
FT /note= "Ser-Gly bridge"  
FT Domain 3..107  
FT /label= kappa\_domain  
XX  
FN WO200018932-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 22-SEP-1999; 99WO-US22045.  
XX  
PR 25-SEP-1998; 98US-0101858.  
PR 19-MAY-1999; 99US-0313942.  
XX  
PA (REGE-) REGENERON PHARM INC.  
XX  
PI Stahl N, Yancopoulos GD;  
XX  
DR WPI; 2000-293165/25.  
XX  
PT Isolated nucleic acid molecule for treating cytokine-related diseases  
PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
PT to form a nonfunctional complex  
XX  
PS Example 4; Fig 13; 152pp; English.  
XX  
CC The invention concerns production of antagonists to any cytokine that  
CC utilizes an alpha specificity determining component, which when combined



CC with the cytokine, binds to a first beta signal transducing component to  
 CC form a non-functional intermediate which then binds to a second beta  
 CC signal transducing component causing beta-receptor dimerization, the  
 CC soluble alpha specificity determining component of the receptor  
 CC (SR-alpha) and the extracellular domain of the first beta signal  
 CC transducing component of the cytokine receptor (beta-1) are combined to  
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the  
 CC cytokine by binding the cytokine to form a non-functional complex. The  
 CC receptor components are shared by cytokines such as the CNTF (ciliary  
 CC neurotrophic factor) family of cytokines. The invention provides the  
 CC basis for the development of IL-6 antagonists, as they show that if, in  
 CC the presence of a ligand, a non-functional intermediate complex,  
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
 CC component, can be formed, it will effectively block the action of the  
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
 CC of the extracellular domains of the alpha specificity determining  
 CC components of their receptors and the extracellular domain of gp130.  
 CC The resultant heterodimers, function as high-affinity traps, rendering  
 CC the cytokine inaccessible to form a signal transducing complex with the  
 CC native membrane-bound forms of their receptor. The nucleic acids and  
 CC polypeptides are useful for treating cytokine-related diseases or  
 CC disorders such as osteoporosis and primary and secondary effects of  
 CC cancer including multiple myeloma or cachexia.

XX Sequence 108 AA;

Query Match 48.6%; Score 107; DB 21; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-92;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 114 GTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
 DB 2 GTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 61  
 QY 174 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 62 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 108

RESULT 8  
 AAR52951  
 ID AAR52951 standard; Protein: 234 AA.

XX AC AAR52951;

XX DT 27-OCT-1994 (first entry)

XX DE Human anti-IgE Mab light chain.

XX KW Human IgE; CH4 region; triggers mediator release;  
 XX KW Mast cells; Monoclonal antibody; allergy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Region 21..128  
 XX FT /label= light chain variable region

XX PN EP592230-A.

XX PD 13-APR-1994.

XX PF 07-OCT-1993; 93EP-0308006.

XX PR 07-OCT-1992; 92JP-0293800.

XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;  
 XX PI Yoshida T;

XX DR WPI; 1994-120330/15.

XX DR N-PSDB; AAQ71872.

XX Human monoclonal anti-IgE peptide antibody - inhibits histamine  
 PT release from mast cells by allergen stimulation, useful for  
 PT preventing allergies  
 XX Claim 3; Page 12; 21pp; English.  
 XX AAR52951 shows the light chain of a human type anti-IgE peptide  
 CC monoclonal antibody which inhibits the signal transmission for  
 CC the release of chemical mediator from mast cells and basophils  
 CC stimulated with allergen. The antibody can be used for the  
 CC prophylaxis and the therapy of allergy.

XX Sequence 234 AA;

Query Match 48.6%; Score 107; DB 15; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 7e-92;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 114 GTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
 DB 128 GTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 187  
 QY 174 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 188 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 9

AAY92196

ID AAY92196 standard; protein: 468 AA.

XX AC AAY92196;

XX DT 01-AUG-2000 (first entry)

XX DE Human IL-6R-alpha-kappa fusion protein.

XX KW IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;  
 XX KW fusion protein; cytostatic; immunomodulator; osteopathic.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Protein 1..358  
 XX FT /label= IL-6R-alpha

XX FT Peptide 359..360

XX FT /note= "Ala-Gly bridge"

XX FT Protein 361..468

XX FT /label= kappa\_domain

XX PN WO200018932-A2.

XX PD 06-APR-2000.

XX PF 22-SEP-1999; 99WO-US22045.

XX PR 25-SEP-1998; 98US-0101858.

XX PR 19-MAY-1999; 99US-0313942.

XX PA (REGG-) REGENERON PHARM INC.

XX PI Stahl N, Yancopoulos GD;

XX DR WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases  
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
 PT to form a nonfunctional complex

XX Example 4; Page -; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that  
CC utilizes an alpha specificity determining component, which when combined  
CC with the cytokine, binds to a first beta signal transducing component to  
CC form a non-functional intermediate which then binds to a second beta  
CC signal transducing component causing beta-receptor dimerization, the  
CC soluble alpha specificity determining component of the receptor  
CC (sr-alpha) and the extracellular domain of the first beta signal  
CC transducing component of the cytokine receptor (beta-1) are combined to  
CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the  
CC cytokine by binding the cytokine to form a non-functional complex. The  
CC receptor components are shared by cytokines such as the CNTF (ciliary  
CC neurotrophic factor) family of cytokines. The invention provides the  
CC basis for the development of IL-6 antagonists, as they show that if, in  
CC the presence of a ligand, a non-functional intermediate complex,  
CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
CC component, can be formed, it will effectively block the action of the  
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
CC of the extracellular domains of the alpha specificity determining  
CC components of their receptors and the extracellular domain of gp130.  
CC The resultant heterodimers, function as high-affinity traps, rendering  
CC the cytokine inaccessible to form a signal transducing complex with the  
CC native membrane-bound forms of their receptor. The nucleic acids and  
CC polypeptides are useful for treating cytokine-related diseases or  
CC disorders such as osteoporosis and primary and secondary effects of  
CC cancer including multiple myeloma or cachexia.

XX SQ Sequence 468 AA;

Query Match 48.6%; Score 107; DB 21; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.3e-91;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
DB 362 GTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 421  
QY 174 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220  
DB 422 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 468

RESULT 10  
AA92192  
ID AAY92192 standard; protein; 727 AA.

XX AC AAY92192;  
XX 01-AUG-2000 (first entry)  
XX Human gp130-kappa domain fusion protein.  
XX gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;  
KW cytotstatic; immunomodulator; osteopathic.  
XX Synthetic.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Protein 1..619  
FT /Label= gp130  
FT Peptide 620..621  
FT /note= "Ser-Gly bridge"  
FT Protein 622..727  
FT /label= IgG1\_kappa\_domain  
XX WO200018932-A2.  
PN 06-APR-2000.  
XX 22-SEP-1999; 99WO-US22045.  
XX 25-SEP-1998; 98US-0101858.  
PR 19-MAY-1999; 99US-0313942.

XX (REGE-) REGENERON PHARM INC.  
PA Stahl N, Yancopoulos GD;  
PI WPI; 2000-293165/25.  
XX Isolated nucleic acid molecule for treating cytokine-related diseases  
XX or disorders encodes a fusion polypeptide capable of binding a cytokine  
XX to form a nonfunctional complex  
XX Example 4; Page -: 152pp; English.  
XX The invention concerns production of antagonists to any cytokine that  
XX utilizes an alpha specificity determining component, which when combined  
XX with the cytokine, binds to a first beta signal transducing component to  
XX form a non-functional intermediate which then binds to a second beta  
XX signal transducing component causing beta-receptor dimerization, the  
XX soluble alpha specificity determining component of the receptor  
XX (sr-alpha) and the extracellular domain of the first beta signal  
XX transducing component of the cytokine receptor (beta-1) are combined to  
XX form heterodimers (sr-alpha:beta-1) that act as antagonist to the  
XX cytokine by binding the cytokine to form a non-functional complex. The  
XX receptor components are shared by cytokines such as the CNTF (ciliary  
XX neurotrophic factor) family of cytokines. The invention provides the  
XX basis for the development of IL-6 antagonists, as they show that if, in  
XX the presence of a ligand, a non-functional intermediate complex,  
XX consisting of the ligand, its alpha receptor and its beta-1 receptor  
XX component, can be formed, it will effectively block the action of the  
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
XX of the extracellular domains of the alpha specificity determining  
XX components of their receptors and the extracellular domain of gp130.  
XX The resultant heterodimers, function as high-affinity traps, rendering  
XX the cytokine inaccessible to form a signal transducing complex with the  
XX native membrane-bound forms of their receptor. The nucleic acids and  
XX polypeptides are useful for treating cytokine-related diseases or  
XX disorders such as osteoporosis and primary and secondary effects of  
XX cancer including multiple myeloma or cachexia.  
XX NB. This sequence was constructed from the gp130 and kappa domain  
XX sequences given in Figures 9 and 13 of the specification.  
XX SQ Sequence 727 AA;  
Query Match 48.6%; Score 107; DB 21; Length 727;  
Best Local Similarity 100.0%; Pred. No. 1.9e-91;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
DB 621 GTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 680  
QY 174 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220  
DB 681 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 727  
RESULT 11  
AAP81028  
ID AAP81028 standard; protein; 106 AA.  
XX AAP81028;  
XX 17-OCT-1990 (first entry)  
XX C region of L chain (chi) of human antibody.  
XX mouse-human chimeric antibody ; anticancer agent;  
KW human common acute lymphocytic leukaemia; ss.  
XX Homo sapiens.  
XX EP255694-A.  
XX

PD 10-FEB-1988.  
 XX 29-JUL-1987; 87EP-0110994.  
 XX 30-JUL-1986; 86JP-0177809.  
 XX (TEIJ ) TEIJIN KK.  
 XX Nishimura Y, Ichikawa Y, Kudo A, Watanabe T;  
 XX WPI; 1988-037653/06.  
 XX Mouse-human chimera antibody -  
 PT used for diagnosis and therapy of human common acute lymphocytic  
 PT leukaemia  
 XX Disclosure; ; p; English.  
 XX The chimeric antibody comprises a C region of human origin linked  
 CC to a V region of mouse origin in both the L and H chains. The mouse  
 CC -derived V region is opt. reactive with human common lymphocytic  
 CC leukaemia antigen.  
 CC See also AAN81358-9, AAN81360, AAN81362-6 and AAP81025-7.  
 XX Sequence 106 AA;  
 SQ

Query Match 48.2%; Score 106; DB 9; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TAAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSTYSLSLTLTKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 220  
 DB 61 KDSTYSLSLTLTKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 106

RESULT 12  
 AAR41687  
 ID AAR41687 standard; Protein; 106 AA.  
 AC AAR41687;  
 XX 20-OCT-1993 (first entry)  
 XX Undefined ORF1 encoded by plasmid pAH4611.  
 XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;  
 KW chain; variable; constant; region; anti-human; transferrin; receptor;  
 KW antibody; brain; capillary; endothelial cell; conjugate; epilepsy;  
 KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;  
 KW Parkinsons disease; Alzheimers disease.  
 XX Synthetic.  
 OS WO9310819-A.  
 XX 10-JUN-1993.  
 XX 24-NOV-1992; 92WO-US10206.  
 XX 26-NOV-1991; 91US-0800458.  
 XX (ALKE-) ALKERMES INC.  
 XX Friden PW;  
 XX WPI; 1993-196742/24.  
 DR N-PSDB; AAQ43845.  
 XX Antibody conjugates specific for transferrin receptor - used

PT for diagnosis and treatment of cancer, AIDS and neurological  
 PT disorders  
 XX Disclosure; Fig 13H; 151pp; English.  
 XX The sequences given in AAR41686-87 represent proteins encoded by the  
 CC expression vector pAH4611. This vector was produced from the plasmid  
 CC PAG4270. PAG4270 is the expression vector for the light chain  
 CC variable region (VL) of the antibody 128.1 which was obtained by PCR  
 CC with leader/J region priming (see also AAQ43842). The vector also  
 CC contains an ampicillin resistance gene, a qpt (mycophenolic acid  
 CC resistance) selected marker, an immunoglobulin H enhancer and an  
 CC intron for V-constant region splicing. Transcription of the CH gene  
 CC is from the VH promoter of the murine 27.44 gene. The cloning of  
 CC of plasmid pSV4271 as an intermediate vector which lacks the promoter  
 CC region. This plasmid was used in conjunction with pAH4602 in the  
 CC production of the chimeric antibody 128.1. 128.1 is an anti-human  
 CC transferrin receptor antibody which binds to the transferrin receptor  
 CC on brain capillary endothelial cells. This antibody may be used in a  
 CC conjugate in which it is linked to a neuropharmaceutical or diagnostic  
 CC agent. The conjugate may be used to treat or prevent neurological  
 CC disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and  
 CC Alzheimers disease. It may also be used for diagnostic methods.  
 XX Sequence 106 AA;  
 SQ

Query Match 48.2%; Score 106; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TAAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSTYSLSLTLTKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 220  
 DB 61 KDSTYSLSLTLTKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 106

RESULT 13  
 AAR43686  
 ID AAR43686 standard; Protein; 106 AA.  
 XX AAR43686;  
 AC AAR43686;  
 XX 25-MAY-1994 (first entry)  
 XX Human kappa constant domain as encoded by pHCMV-KR.  
 XX Human; immunoglobulin; constant; region; humanised; P-selectin; light;  
 KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;  
 KW monoclonal; PBL 3; CDR; complementarity determining region; leukocyte;  
 KW expression vector; coexpression; pHCMV-1748RHA-gamma1CI-dhfr; epitope;  
 KW pHCMV-1748RLA-KR-neo; PBL 3/Humanised version A; vascular endothelium;  
 KW pHCMV-1747CH-gamma1CI-neo; pHCMV-1747-CL-KR-neo; PBL 3 chimera;  
 KW acute lung injury; ischaemia reperfusion injury; inflammation.  
 XX Homo sapiens.  
 OS WO9321956-A.  
 XX 11-NOV-1993.  
 XX 04-MAY-1993; 93WO-US04274.  
 XX 05-MAY-1992; 92US-0880196.  
 XX (CYTE-) CYTEL CORP.  
 XX Chestnut RW, Paulson JC, Polley MJ;  
 XX WPI; 1993-368423/46.  
 DR

DR N-PSDB; AAQ51548.  
 XX  
 XX Anti-P-selectin antibody for ischaemia acute lung injury treatment -  
 PT useful to treat inflammation and pathological conditions of  
 PT Inter cellular adhesion by competitive inhibition assays  
 XX  
 PS Example 10; Fig 10; 82pp; English.  
 XX  
 XX The sequences given in AAR43685-86 represent human immunoglobulin  
 CC constant regions which were used in the production of the humanised  
 CC P-selectin blocking antibody, along with the heavy and light chain  
 CC variable region coding sequences of the murine monoclonal antibody  
 CC PBL.3, given in AAR43687-88. The CDRs from PBL.3 heavy and light  
 CC chains were substituted for the CDRs of human heavy and light chains.  
 CC The humanised variable regions were inserted into expression vectors.  
 CC By coexpression of appropriate combinations of heavy and light  
 CC chains, several humanised antibodies can be expressed. Coexpression  
 CC of pHCMV-1748RIA-gamma1C1-dhfr and pHCMV-1748RLA-KR-neo gives rise  
 CC to the PBL.3/Humanised version A. Coexpression of pHCMV-1747CH-  
 CC gammaC1-neo and pHCMV-1747-CL-KR-neo gives rise to the PBL.3 chimera.  
 CC These humanised antibodies selectively bind epitopes on P-selectin and  
 CC block adhesion of leukocytes to the vascular endothelium. They may be  
 CC used to treat inflammatory and thrombotic diseases and other  
 CC pathological conditions involving P-selectin and antibodies to it, esp.  
 CC acute lung injury and ischaemia reperfusion injury.  
 XX  
 SQ Sequence 106 AA;  
 Query Match 48.2%; Score 106; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
 Db 1 TVAAPSVFIFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
 RESULT 14  
 AAW37347  
 ID AAW37347 standard; Protein; 106 AA.  
 AC AAW37347;  
 XX  
 XX 11-MAY-1998 (first entry)  
 DT  
 DE Immunoglobulin C-kappa region.  
 XX  
 XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;  
 KW gene amplification; immunotherapy; therapy; immunoglobulin;  
 KW C-kappa; constant region.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9741244-A1.  
 PN  
 XX 06-NOV-1997.  
 PD  
 XX 25-APR-1997; 97WO-US07039.  
 PF  
 XX 06-DEC-1996; 96US-0761277.  
 PR  
 XX 01-MAY-1996; 96US-0644664.  
 XX  
 XX (GENI-) GENITOPE CORP.  
 PA  
 XX Denney DW;  
 PI  
 XX WPI; 1997-549743/50.  
 DR N-PSDB; AAT97190.  
 XX

PT Multivalent vaccine to treat B cell lymphoma or leukaemia -  
 PT comprises at least 2 different recombinant variable regions of  
 XX immunoglobulin molecules derived from B cell lymphoma cells  
 PS Example 10; Page 127-128; 177pp; English.  
 XX  
 CC This protein comprises an immunoglobulin (Ig) C-kappa region.  
 CC The invention provides a method for the production of tumour-  
 CC specific Ig derived from a B-cell lymphoma patient. In the novel  
 CC method, expression plasmids containing the patient's VH region(s)  
 CC joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)  
 CC sequence and expression plasmids containing the patient's VL  
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2  
 CC (see AAT97191) sequence are cotransfected along with a selectable and  
 CC amplifiable marker into a cell line (e.g. BW5147.G.1.4), and  
 CC transfected cells are then subjected to selection and amplification.  
 CC The method permits the production of a multivalent vaccine which  
 CC reflects the degree of somatic variation found within the patient's  
 CC tumour. These novel multivalent vaccines provide superior vaccines  
 CC for the treatment of B-cell lymphoma.  
 XX  
 SQ Sequence 106 AA;  
 Query Match 48.2%; Score 106; DB 18; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
 Db 1 TVAAPSVFIFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
 RESULT 15  
 AAW59622  
 ID AAW59622 standard; Protein; 106 AA.  
 XX  
 XX AAW59622;  
 XX  
 XX 12-OCT-1998 (first entry)  
 DT  
 XX  
 DE Anti-RSV F protein Hu19 MAB light chain constant region.  
 XX  
 KW Monoclonal antibody; human; Hu19C; Hu19D; engineered antibody; RSV;  
 KW respiratory syncytial virus; complementarity determining region;  
 KW CDR; infection; immunotherapy; therapy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9819704-A1.  
 PN  
 XX 14-MAY-1998.  
 PD  
 XX 23-OCT-1997; 97WO-US19203.  
 PF  
 XX 01-NOV-1996; 96US-0030149.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA  
 XX Deen KC, Dillon SB, Porter TG, Sweet RW;  
 PI  
 XX WPI; 1998-286600/25.  
 DR  
 XX Monoclonal antibodies reactive with Respiratory Syncytial Virus -  
 PT useful for detection, prevention and treatment of RSV infections  
 PT  
 XX Disclosure; Fig 3; 109pp; English.  
 PS  
 XX This is the amino acid sequence of the light chain constant region  
 CC (C kappa) of constructs 19C and 19D of novel human monoclonal  
 CC

CC antibodies (Mabs) reactive with the fusion (F) protein of  
CC respiratory syncytial virus (RSV). Hui9A, Hui9B, Hui9C and Hui9D  
CC Mabs are claimed. These are reshaped human antibodies comprising a  
CC heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and  
CC a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).  
CC Such engineered antibodies are neutralising; they inhibit virus  
CC growth in vitro and in vivo in animal models of RSV infection.  
CC They can be used in the detection, prevention and passive  
CC immunotherapy of RSV infection. Nucleic acids encoding the human  
CC Mabs, recombinant plasmids (see AAV41427-33) and host cells (e.g.  
CC COS, CHO, myeloma) are provided.  
xx  
SQ Sequence 106 AA;  
Query Match 48.2%; Score 106; DB 19; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVEIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVEIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
QY 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106

Search completed: October 9, 2002, 19:23:00  
Job time : 24.5714 secs



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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 8.9759 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 220  
Sequence: 1 EIVLTQSLPLVPVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

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Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	48.2	106	2	US-08-378-939-40
2	106	48.2	106	2	US-08-761-277A-49
3	106	48.2	106	3	US-08-444-644-26
4	106	48.2	106	4	US-08-232-246A-26
5	106	48.2	107	1	US-08-422-101-8
6	106	48.2	107	1	US-08-422-091-8
7	106	48.2	107	2	US-08-422-092-8
8	106	48.2	107	2	US-08-788-800-5
9	106	48.2	107	3	US-08-422-093-8
10	106	48.2	107	3	US-08-422-112-8
11	106	48.2	213	3	US-08-630-820-6
12	106	48.2	213	3	US-08-397-411-12
13	106	48.2	214	1	US-08-458-516-12
14	106	48.2	214	2	US-07-934-373C-24
15	106	48.2	214	2	US-07-934-373C-39
16	106	48.2	214	2	US-07-934-373C-40
17	106	48.2	214	2	US-08-480-753-6
18	106	48.2	214	2	US-08-788-800-11
19	106	48.2	214	3	US-09-041-889-11
20	106	48.2	214	3	US-08-437-642B-24
21	106	48.2	214	3	US-08-437-642B-39
22	106	48.2	214	3	US-08-437-642B-40
23	106	48.2	214	3	US-08-837-058-11
24	106	48.2	214	3	US-09-097-309-2
25	106	48.2	214	3	US-08-397-411-5
26	106	48.2	214	4	US-09-097-171A-2
27	106	48.2	214	4	US-09-247-352-4

28	106	48.2	214	4	US-09-679-397-1	Sequence 1, Appli
29	106	48.2	214	5	PCT-US93-07832-24	Sequence 24, Appl
30	106	48.2	214	5	PCT-US93-07832-39	Sequence 39, Appl
31	106	48.2	214	5	PCT-US93-07832-40	Sequence 40, Appl
32	106	48.2	215	2	US-08-480-753-8	Sequence 8, Appli
33	106	48.2	218	2	US-08-887-352B-13	Sequence 13, Appl
34	106	48.2	218	2	US-08-887-352B-15	Sequence 15, Appl
35	106	48.2	218	2	US-08-887-352B-17	Sequence 17, Appl
36	106	48.2	218	2	US-08-887-352B-19	Sequence 19, Appl
37	106	48.2	218	2	US-08-887-352B-24	Sequence 24, Appl
38	106	48.2	218	3	US-08-466-151-9	Sequence 9, Appli
39	106	48.2	218	4	US-09-109-207C-13	Sequence 13, Appl
40	106	48.2	218	4	US-09-109-207C-15	Sequence 15, Appl
41	106	48.2	218	4	US-09-109-207C-17	Sequence 17, Appl
42	106	48.2	218	4	US-09-109-207C-19	Sequence 19, Appl
43	106	48.2	218	4	US-09-109-207C-24	Sequence 24, Appl
44	106	48.2	218	4	US-09-282-505-1	Sequence 1, Appli
45	106	48.2	218	4	US-09-054-255-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-378-939-40  
; Sequence 40, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROWE, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-40

Query Match 48.2%; Score 106; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 115 TVAAPSVFIFPPSDQLKSGTASVVCCLNFFYPREAKVKQVDNALQSGNSQESVTEQDS 174  
|||||  
Db 1 TVAAPSVFIFPPSDQLKSGTASVVCCLNFFYPREAKVKQVDNALQSGNSQESVTEQDS 60

Qy 175 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

## RESULT 2

US-08-761-277A-49  
; Sequence 49, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761,277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-761-277A-49

Query Match 48.2%; Score 106; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 60

Qy 175 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

## RESULT 3

US-08-444-644-26  
; Sequence 26, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-444-644-26

Query Match 48.2%; Score 106; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 60

Qy 175 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

## RESULT 4

US-08-232-246A-26  
; Sequence 26, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.246A  
FILING DATE: 04-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-232-246A-26

Query Match 48.2%; Score 106; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 1 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
QY 175 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 5  
US-08-422-101-8  
Sequence 8, Application US/08422101  
Patent No. 5739277  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,101  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-101-8  
Query Match 48.2%; Score 106; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 2 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
QY 175 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
RESULT 6  
US-08-422-091-8  
Sequence 8, Application US/08422091  
Patent No. 5747035  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,091  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-422-091-8

Query Match 48.2%; Score 106; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 174  
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Db 2 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 61  
|||||

Qy 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
|||||

Db 62 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

RESULT 7

US-08-422-092-8  
; Sequence 8, Application US/08422092  
; Patent No. 5869046  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,092  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-422-092-8

Query Match 48.2%; Score 106; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 174  
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Db 2 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 61  
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Qy 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
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Db 62 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 8

US-08-788-800-5

; Sequence 5, Application US/08788800  
; Patent No. 5914112  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; APPLICANT: Thomas, G. Roger  
; APPLICANT: Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/788,800  
; FILING DATE: 22-Jan-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0987r1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-788-800-5

Query Match 48.2%; Score 106; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 174  
|||||

Db 2 TAAAPSVFIPPSPDEQLKSGTASVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 61  
|||||

Qy 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
|||||

Db 62 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

RESULT 9

US-08-422-093-8  
; Sequence 8, Application US/08422093  
; Patent No. 6096871  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,093  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-093-8

Query Match 48.2%; Score 106; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
Db 2 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
|||||  
QY 175 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
Db 62 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

RESULT 10  
US-08-422-112-8  
Sequence 8, Application US/08422112  
Patent No. 6121022  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,112  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881

TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-112-8  
Query Match 48.2%; Score 106; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
Db 2 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
|||||  
QY 175 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
Db 62 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||  
RESULT 11  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: Oppen, Martin  
APPLICANT: Bosslet, Klaus  
APPLICANT: Czech, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-6  
Query Match 48.2%; Score 106; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.7e-90;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-24

Query Match 48.2%; Score 106; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 109 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 168

QY 175 KSTYSLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 169 KSTYSLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: October 9, 2002, 19:26:36
Job time : 8.97959 secs

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; US-07-934-373C-39
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-39

Query Match 48.2%; Score 106; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 109 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 168

QY 175 KSTYSLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 169 KSTYSLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: October 9, 2002, 19:26:36
Job time : 8.97959 secs

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RESULT 15
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:

```



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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:19:35 ; Search time 11.7857 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 220  
Sequence: 1 EIVLTQSLPLSVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	48.2	106	1 K3HU	Ig kappa chain C r
2	106	48.2	215	2 JE0244	Ig kappa chain NIG
3	106	48.2	215	2 JE0242	Ig kappa chain NIG
4	106	48.2	215	2 JE0243	Ig kappa chain C r
5	99	45.0	99	2 S26653	JC-kappa protein -
6	82	37.3	135	2 S52059	Ig kappa chain C r
7	75	34.1	99	2 A37927	Ig kappa chain C r
8	70	31.8	216	2 JE0241	Ig kappa chain An3
9	59	26.8	215	2 A23746	Ig kappa chain V-I
10	31	14.1	112	2 S58207	Ig light chain V r
11	31	14.1	112	2 S58206	Ig light chain V r
12	31	14.1	117	1 K2HUGM	Ig kappa chain pre
13	31	14.1	123	2 S40319	Ig kappa chain V r
14	31	14.1	132	2 S26882	Ig kappa chain V r
15	31	14.1	135	2 S40342	Ig kappa chain - h
16	31	14.1	136	2 S40357	Ig kappa chain V-I
17	30	13.6	114	2 S40375	Ig kappa chain - h
18	28	12.7	113	1 K2HUTW	Ig kappa chain V-I
19	27	12.3	100	2 S24681	Ig kappa chain - h
20	27	12.3	125	2 S40356	Ig kappa chain - h
21	27	12.3	126	2 S40339	Ig kappa chain - h
22	26	11.8	112	1 K2HUML	Ig kappa chain V-I
23	26	11.8	121	2 S40371	Ig kappa chain V r
24	24	10.9	120	2 A49043	Ig kappa chain V r
25	23	10.5	115	1 K2HUCM	Ig kappa chain V-I
26	23	10.5	121	2 S24205	Ig kappa chain V r
27	23	10.5	127	2 S40323	Ig kappa chain - h
28	23	10.5	130	2 S40321	Ig kappa chain - h
29	22	10.0	87	2 S34091	Ig kappa chain V r

A:Residues: 1-56, 'O', 58-106 <H12>  
R:Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <TIT>  
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507  
A:Contents: Waldenstrom's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <KOH>  
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Note: allotype Inv(3)  
R:Steiner, Y.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-References: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into larger complexes  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 48.2%; Score 106; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 1 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 61 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
|||||

RESULT 2  
JE0244  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL amyloidosis:  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215  
|||||

RESULT 4  
JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H. submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL amyloidosis:  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215  
|||||

RESULT 5  
S26653  
Ig kappa chain C region - chimpanzee (fragment)

Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215  
|||||

RESULT 3  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215  
|||||

RESULT 4  
JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H. submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL amyloidosis:  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215  
|||||

RESULT 5  
S26653  
Ig kappa chain C region - chimpanzee (fragment)



C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C:Accession: S26653  
R:Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybridomas 1, 23-26, 1990  
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
A:Reference number: S26652; MUID:91355693  
A:Accession: S26653  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-99 <EHR>  
A:Cross-references: EMBL:X65287  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 99; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.5e-91;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 175 KDSTYLSSTLTLSKADYEKHKVACEVTHQGLSSPVTK 213  
Db 61 KDSTYLSSTLTLSKADYEKHKVACEVTHQGLSSPVTK 99

RESULT 6  
S52059  
JC-kappa protein - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Sep-2000  
C:Accession: S52059  
R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Sacland, S.;  
EMBO J. 13, 5937-5943, 1994  
A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c  
A:Reference number: S52059; MUID:95112804  
A:Accession: S52059  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <FRA>  
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 37.3%; Score 82; DB 2; Length 135;  
Best Local Similarity 100.0%; Pred. No. 5.2e-74;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 30 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 89

QY 175 KDSTYLSSTLTLSKADYEKHK 196  
Db 90 KDSTYLSSTLTLSKADYEKHK 111

RESULT 7  
A37927  
Ig kappa chain C region (allotype Inv(1.2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C:Accession: A37927  
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: A37927  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 34.1%; Score 75; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.8e-67;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 181  
Db 1 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 60

QY 182 SSTLTLSKADYEKHK 196  
Db 61 SSTLTLSKADYEKHK 75

RESULT 8  
JE0241  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0241  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 31.8%; Score 70; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 7.1e-62;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 111 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 170

QY 175 KDSTYLSST 184  
Db 171 KDSTYLSST 180

RESULT 9  
A23746  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immun  
A:Reference number: A23746; MUID:91131575  
A:Accession: A23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 59; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.6e-51;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LINFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYA 199  
Db 136 LINFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYA 194

RESULT 10

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F;1-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F;20-99/Domain: immunoglobulin homology <IMM>  
F;27-97/Disulfide bonds: #status predicted

Query Match 14.1%; Score 31; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASISCRSSQSLLHSGY 35  
|||||  
Db 9 TQSPLSLPVTPGEPASISCRSSQSLLHSGY 39  
|||||

RESULT 13  
S40319  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40319  
R;Kleip, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891  
A;Accession: S40319  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-123 <LE>  
A;Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;26-105/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 31; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASISCRSSQSLLHSGY 35  
|||||  
Db 15 TQSPLSLPVTPGEPASISCRSSQSLLHSGY 45  
|||||

RESULT 14  
S26882  
Ig kappa chain V region (V607) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C;Accession: S26882  
R;Weichhold, G.M.; Klobbeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A;Title: Megabase inversions in the human genome as physiological events.  
A;Reference number: S26882; MUID:90370099  
A;Accession: S26882  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-132 <WEI>  
A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367  
C;Genetics:

A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 31; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3.6e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASISCRSSQSLLHSGY 35  
|||||

Db 25 TQSPSLPVTGPASPISCRSSQSLHSHNGY 55

RESULT 15

S40342

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40342

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891

A:Accession: S40342

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <KLE>

A:Cross-references: EMBL:X72452; NID:g441372; PID:g441373

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:29-108/Domain: immunoglobulin homology <IMM>

Query Match

14.18; Score 31; DB 2; Length 135;

Best Local Similarity 100.0%; Pred. No. 3.6e-23;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPASPISCRSSQSLHSHNGY 35

|||||

Db 18 TQSPSLPVTGPASPISCRSSQSLHSHNGY 48

Search completed: October 9, 2002, 19:25:52

Job time : 12.7857 secs



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OM protein - protein search, using sw model

Run On: October 9, 2002, 19:13:25 ; Search time 6.73469 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLSPVTGPASPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	48.2	106	1 KAC_HUMAN	P01834
2	31	14.1	117	1 KV2E_HUMAN	P06309
3	28	12.7	113	1 KV2D_HUMAN	P01617
4	26	11.8	112	1 KV2C_HUMAN	P01616
5	23	10.5	115	1 KV2A_HUMAN	P01614
6	22	10.0	112	1 KV2D_MOUSE	P01629
7	22	10.0	113	1 KV2E_MOUSE	P03976
8	20	9.1	113	1 KV2F_MOUSE	P01630
9	17	7.7	133	1 KV2F_HUMAN	P06310
10	14	6.4	108	1 KV1_CANFA	P01618
11	13	5.9	107	1 KV1D_HUMAN	P01596
12	11	5.0	113	1 KV2B_HUMAN	P01615
13	11	5.0	113	1 KV2G_MOUSE	P01631
14	10	4.5	109	1 LV1F_HUMAN	P04208
15	10	4.5	109	1 LV2E_HUMAN	P01708
16	10	4.5	111	1 LV1A_HUMAN	P01699
17	10	4.5	111	1 LV2F_HUMAN	P01709
18	10	4.5	111	1 LV2G_HUMAN	P01710
19	10	4.5	111	1 LV2H_HUMAN	P01712
20	10	4.5	111	1 LV6C_HUMAN	P06317
21	10	4.5	112	1 LV1B_HUMAN	P01700
22	10	4.5	112	1 LV6A_HUMAN	P01721
23	10	4.5	114	1 KV4A_HUMAN	P01625
24	10	4.5	120	1 KV2B_MOUSE	P01627
25	10	4.5	131	1 KV4O_HUMAN	P06312
26	10	4.5	133	1 KV4B_HUMAN	P06313
27	10	4.5	134	1 KV4C_HUMAN	P06314
28	9	4.1	106	1 KACA_RAT	P01836
29	9	4.1	106	1 KACB_RAT	P01835
30	9	4.1	106	1 KACD_MOUSE	P01837
31	9	4.1	108	1 KV5P_MOUSE	P01649
32	9	4.1	112	1 KV2A_MOUSE	P01626
33	9	4.1	113	1 KV2C_MOUSE	P01628

#### ALIGNMENTS

##### RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (hence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press,			
RL	New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

P06319 homo sapien  
P01621 homo sapien  
P01839 oryctolagus  
P01675 mus musculus  
P01676 mus musculus  
P01677 mus musculus  
P01678 mus musculus  
P01679 mus musculus  
P01597 homo sapien  
P00362 homo sapien  
P01620 homo sapien  
P01622 homo sapien

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
RJ J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains.";
RJ Science 169:56-59(1970).
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
DR EMBL; J00241; AAA58989.1; -;
DR EMBL; V00557; CAA23823.1; -;
DR PIR; A02116; K3HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147200; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT VARIANT 83 83 * V -> L (IN INV(1,2) MARKER).
FT /FTID=VAR_003897.
FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
Query Match 48.2%; Score 106; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e-103; Mismatches 0; Gaps 0;
Matches 106; Conservative 0; Indels 0;
QY 115 TVAAPSVFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
DB 1 TVAAPSVFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 175 KDSYSLSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 220
DB 61 KDSYSLSTLTLSKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 106
RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
-1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RJ Nature 309:73-76(1984).
RL Nature 309:73-76(1984).
CC -----
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CC -----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Query Match 14.1%; Score 31; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQSPLSLPVTPGEPASISCRSSQSLHNSGY 35
DB 9 TQSPLSLPVTPGEPASISCRSSQSLHNSGY 39
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
Primary amyloidosis.";
RJ Biochemistry 12:3763-3780(1973).
RN [2]
SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
RJ J. Clin. Invest. 52:1276-1281(1973).
RN [1]
-1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
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CC      WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC      -I- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC      PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC      -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC      MARKER.
DR      PIR: A01888; K2HUTW.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KW      Immunoglobulin V region; Bence-Jones protein; Anyloid.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 40 54 FRAMEWORK-2.
FT      DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 62 93 FRAMEWORK-3.
FT      DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 103 112 FRAMEWORK-4.
FT      DISULFID 23 93 BY SIMILARITY.
FT      NON_TER 113 113
SQ      SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 12.7%; Score 28; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-22; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY      5 TQSPSLVPTGPEPASISCRSSQSLHS 32
Db      5 TQSPSLVPTGPEPASISCRSSQSLHS 32

RESULT 4
KV2C_HUMAN
ID      KV2C_HUMAN STANDARD; PRT; 112 AA.
AC      P01616;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region MLL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RA      Dreyer W.J., Gray W.R., Hood L.E.;
RA      SEQUENCE.
RT      "The genetic, molecular, and cellular basis of antibody formation:
RT      some facts and a unifying hypothesis.";
RL      Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC      -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC      -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      PIR: A01887; K2HUML.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 39 53 FRAMEWORK-2.
FT      DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 61 92 FRAMEWORK-3.
FT      DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 102 111 FRAMEWORK-4.
FT      DISULFID 23 92 BY SIMILARITY.
FT      NON_TER 112 112
SQ      SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 11.8%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVLTQSPSLVPTGPEPASISCRSSQ 27

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Db      2 IVLTQSPSLVPTGPEPASISCRSSQ 27

RESULT 5
KV2A_HUMAN
ID      KV2A_HUMAN STANDARD; PRT; 115 AA.
AC      P01614;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region Cum.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RA      SEQUENCE.
RA      MEDLINE=68242259; PubMed=5586923;
RA      Hilschmann N.;
RT      "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT      type).";
RL      Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN      [2]
RP      REVISIONS TO 50; 52; 96 AND 97.
RX      MEDLINE=70063440; PubMed=4188189;
RA      Hilschmann N.;
RT      "Molecular basis of antibody formation.";
RL      Naturwissenschaften 56:195-205(1969).
CC      -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC      -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      PIR: A01885; K2HUCM.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DISULFID 24 95 BY SIMILARITY.
FT      NON_TER 115 115
SQ      SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 10.5%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PLSLPVTPGEPASISCRSSQSL 30
Db      9 PLSLPVTPGEPASISCRSSQSL 31

RESULT 6
KV2D_MOUSE
ID      KV2D_MOUSE STANDARD; PRT; 112 AA.
AC      P01629;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region 2S1.3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RA      SEQUENCE.
RA      MEDLINE=83055101; PubMed=7141411;
RA      Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RT      "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
RT      the group A streptococcal polysaccharide.";
RL      Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC      -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC      ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR      PIR: A01911; KVMSS1.
DR      InterPro: IPR003006; Ig_MHC.

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KV2F\_MOUSE STANDARD; PRT; 113 AA.

ID KV2F\_MOUSE AC P01630; 21-JUL-1986 (Rel. 01, Created)

DT DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE DE Ig kappa chain V-II region FS34.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

SEQUENCE.

RP MEDLINE=83256427; PubMed=6409088;

RX Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;

RA "A new isotype sequence (V kappa 27) of the variable region of kappa-

RT light chains from a mouse hybridoma-derived anti-(streptococcal group

RT A polysaccharide) antibody containing an additional cysteine residue.

RT Application of the dimethylaminobenzene isothiocyanate technique

RT for the isolation of peptides."

RL Biochem. J. 211:173-180(1983)."

CC -I- MISCELLANEOUS; THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL

CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

DR PTR: A01913; KVM57S.

DR InterPro: IPR003006; Iq\_MHC.

DR InterPro: IPR003596; Iq\_V.

DR Pfam: PF00047; Iq; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 40 54 FRAMEWORK-2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 62 93 FRAMEWORK-3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 103 112 FRAMEWORK-4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON\_TER 113 113

SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 9.1%; Score 20; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 FTLRISRVEADVGYYCMQ 95  
|||||  
DB 76 FTLRISRVEADVGYYCMQ 95  
|||||

RESULT 9

KV2F\_HUMAN STANDARD; PRT; 133 AA.

ID KV2F\_HUMAN AC P06310;

DT DT 01-JAN-1988 (Rel. 06, Created)

DT DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE DE Ig kappa chain V-II region RPMI 6410 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041852; PubMed=2997711;

RA Klobeck H.G., Meindl A., Combario G., Solomon A., Zachau H.G.;

RT "Human immunoglobulin kappa light chain genes of subgroups II and

RT III.";

RL Nucleic Acids Res. 13:6499-6513(1985).

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DR	EMBL; Z00020; CAA77315.1; -.
DR	PIR; A01890; K2HURP.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 133
FT	DOMAIN 21 43
FT	DOMAIN 44 59
FT	DOMAIN 60 74
FT	DOMAIN 75 81
FT	DOMAIN 82 113
FT	DOMAIN 114 122
FT	DOMAIN 123 132
FT	DISULFID 43 113
FT	NON_TER 133 133
SQ	SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64:

RESULT 10			
KVL_CANFA	KVL_CANFA	PRT;	108 AA.
ID	KVL_CANFA	STANDARD;	
AC	P01618;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DE	19-JUL-1999 (Rel. 38, Last annotation update)		
DE	1g kappa chain V region GOM.		
OS	Canis familiaris (Dog).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=79026193; PubMed=100411;		
RA	Wasserman R.L., Capra J.D.;		
RT	"The amino acid sequence of the light chain variable region of a		
RT	canine myeloma immunoglobulin: evidence that the VK subgroups		
RT	predated mammalian speciation.";		
RL	Immunochimistry 15:303-305(1978).		
CC	-!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA		
CC	CHAINS.		
CC	-!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF		
CC	THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.		
CC	PIR; A01907; K2DGM.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
KW	Immunoglobulin V region.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34	FRAMEWORK-1.	
FT	DOMAIN 35 49	COMPLEMENTARITY-DETERMINING-1.	
FT	DOMAIN 50 56	FRAMEWORK-2.	
FT	DOMAIN 57 88	COMPLEMENTARITY-DETERMINING-2.	
FT	DOMAIN 89 97	FRAMEWORK-3.	
FT	DOMAIN 98 107	COMPLEMENTARITY-DETERMINING-3.	
FT	DISULFID 23 88	FRAMEWORK-4.	
FT	NON_TER 108 108	BY SIMILARITY.	
SQ	SEQUENCE 108 AA; 112005 MW;	02FEC498C47A3126 CRC64;	

RESULT 12	
KV2B_HUMAN	
ID	KV2B_HUMAN
AC	P01615;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-II region FR.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=76253627; PubMed=821524;
RA	Riesen W.F., Jaton J.-C.;
RT	"Variable region sequence of the light chain from a Waldenstrom's IgM
RF	with specificity for phosphorylcholine.";
RL	Biochemistry 15:3829-3833(1976).
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC	MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

RESULT 12	
KV2B_HUMAN	
ID	KV2B_HUMAN
AC	P01615;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-II region FR.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=76253627; PubMed=821524;
RA	Riesen W.F., Jaton J.-C.;
RT	"Variable region sequence of the light chain from a Waldenstrom's IgM with specificity for phosphorylcholine.";
RL	Biochemistry 15:3829-3833(1976).
CC	-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

```
DR PIR; A01886; K2HUPR.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 5.0%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AEDGVVYCMQ 95
Db 85 AEDGVVYCMQ 95
|||||

RESULT 13
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
CC PIR; A01914; KWS26.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 5.0%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQL 29
Db 19 ASISCRSSQL 29
|||||

us-09-822-698a-24.rsp

RESULT 14
LV1F_HUMAN
ID LV1F_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; L1HUWA.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109
FT DISULFID 22 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 4.5%; Score 10; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70
Db 57 SGVPDRFSGS 66
|||||

RESULT 15
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
sequence of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
MARKERS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01974; L2HUBR.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT DISULFID 22 90
BY SIMILARITY.

us-09-822-698a-24.rsp
```

FT SITE 91 91 APPEARS TO BE A FREE BUT UNREACTIVE  
FT NON\_TER 109 109 SULFHYDRYL GROUP.  
SQ SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;  
Query Match 4.5%; Score 10; DB 1; Length 109;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 SGVPRFRSGS 70  
Db 58 SGVPRFRSGS 67

Search completed: October 9, 2002, 19:23:37  
Job time : 7.73469 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 18.801 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLVTPGPAS.....EVTHOGLSPVTKSFNRGEC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp Unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	7.7	114	4	Q9UL80	Q9ul80 homo sapien
2	14	6.4	108	4	Q9UL83	Q9ul83 homo sapien
3	13	5.9	109	4	Q9UL86	Q9ul86 homo sapien
4	11	5.0	104	11	Q9UL82	Q9j182 mus musculus
5	11	5.0	116	4	Q96PF6	Q96pf6 homo sapien
6	10	4.5	107	4	Q9UL81	Q9ul81 homo sapien
7	10	4.5	108	4	Q96SB0	Q96sb0 homo sapien
8	10	4.5	112	4	Q96JD2	Q96jd2 homo sapien
9	10	4.5	112	4	Q96JDI	Q96jdi homo sapien
10	10	4.5	116	4	Q96JDO	Q96jdo homo sapien
11	10	4.5	235	11	Q91WI2	Q91wi2 mus musculus
12	10	4.5	236	4	Q96E61	Q96e61 homo sapien
13	10	4.5	238	11	Q99M37	Q99m37 mus musculus
14	9	4.1	211	11	Q91XL0	Q91xl0 mus musculus
15	9	4.1	214	11	Q98JA5	Q98ja5 mus musculus
16	9	4.1	233	11	Q91WS9	Q91ws9 mus musculus

17	9	4.1	234	11	Q91WF8	Q91wf8 mus musculus
18	8	3.6	97	11	Q9JL76	Q9j176 mus musculus
19	8	3.6	109	4	Q9UL78	Q9ul78 homo sapien
20	8	3.6	258	16	Q98DX9	Q98dx9 rhizobium 1
21	8	3.6	278	11	Q921K1	Q921k1 mus musculus
22	8	3.6	337	6	Q95M34	Q95m34 equus cabal
23	8	3.6	468	11	Q99L31	Q99l31 mus musculus
24	8	3.6	473	11	Q9DL84	Q9dl84 mus musculus
25	8	3.6	473	11	Q99L25	Q99l25 mus musculus
26	8	3.6	473	11	Q91Z05	Q91z05 mus musculus
27	8	3.6	480	4	Q96JV4	Q96jv4 homo sapien
28	8	3.6	490	16	P74334	P74334 synochocyst
29	7	3.2	75	16	O50840	O50840 borrelia bu
30	7	3.2	77	12	Q84508	Q84508 paramecium
31	7	3.2	95	16	Q9RVD5	Q9rvd5 deinococcus
32	7	3.2	99	11	Q9JL74	Q9j174 mus musculus
33	7	3.2	105	17	Q96ZF1	Q96zf1 sulfolobus
34	7	3.2	106	5	Q9U410	Q9u410 schistosoma
35	7	3.2	107	4	Q9NSD6	Q9nsd6 homo sapien
36	7	3.2	107	4	Q96SA9	Q96sa9 homo sapien
37	7	3.2	107	11	Q9ERZ9	Q9erz9 mus musculus
38	7	3.2	108	4	Q9UL79	Q9ul79 homo sapien
39	7	3.2	108	4	Q9UL77	Q9ul77 homo sapien
40	7	3.2	108	4	Q9UL70	Q9ul70 homo sapien
41	7	3.2	111	11	Q920S9	Q920s9 mus musculus
42	7	3.2	116	16	Q92CR3	Q92cr3 listeria in
43	7	3.2	130	4	Q9NP29	Q9np29 homo sapien
44	7	3.2	159	16	Q9RXP4	Q9rx14 deinococcus
45	7	3.2	164	5	Q9GN43	Q9gn43 schistosoma

#### ALIGNMENTS

RESULT 1  
Q9UL80  
ID Q9UL80 PRELIMINARY; PRT; 114 AA.  
AC Q9UL80;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035034; AAD56270.1; -  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
FT NON\_TER 1  
FT NON\_TER 114  
SQ SEQUENCE 114 AA; 12175 MW; 070E31E210D1CB01 CRC64;

Query Match 7.7%; Score 17; DB 4; Length 114;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 ISRVEADVGYYCMQ 96

|||||

Db 80 ISRVEADVGYYCMQ 96

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RESULT 2
Q9UL83 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 6.4%; Score 14; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 PTFGPGTKVDIKR 113
Db 95 PTFGPGTKVDIKR 108
|||||

RESULT 3
Q9UL86 ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 5.9%; Score 13; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 FTFGPGTKVDIKR 113
Db 97 FTFGPGTKVDIKR 109
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RESULT 4
Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 104
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 5.0%; Score 11; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQSL 29
Db 11 ASISCRSSQSL 21
|||||

RESULT 5
Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNKL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1 116
FT NON_TER 116 116
```

SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 5.0%; Score 11; DB 4; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 PFTFGPGTKVD 110  
|||||

Db 95 PFTFGPGTKVD 105

## RESULT 6

Q9UL81 ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -;  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Iq\_MHC.  
DR InterPro; IPR003596; Iq\_V.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 107 105

SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
Query Match 4.5%; Score 10; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TFGPGTKVDI 111  
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Db 96 TFGPGTKVDI 105

## RESULT 7

Q96SB0 ID Q96SB0 PRELIMINARY; PRT; 108 AA.  
AC Q96SB0;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96394; AAB68783.1; -;

FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 4.5%; Score 10; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFGS 70  
|||||

Db 57 SGVDPDRFGS 66

## RESULT 8

Q96JD2 ID Q96JD2 PRELIMINARY; PRT; 112 AA.  
AC Q96JD2;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX TISSUE-BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region NEG."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267873; AAK58585.1; -;

FT NON\_TER 1  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;  
Query Match 4.5%; Score 10; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFGS 70  
|||||

Db 57 SGVDPDRFGS 66

## RESULT 9

Q96JD1 ID Q96JD1 PRELIMINARY; PRT; 112 AA.  
AC Q96JD1;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX TISSUE-BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region PIP."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267874; AAK58586.1; -;

FT NON\_TER 1  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;  
Query Match 4.5%; Score 10; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFGS 70  
|||||

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Db 57 SGVDPDFSGS 66
RESULT 10
Q96JD0 PRELIMINARY; PRT; 116 AA.
ID Q96JD0;
AC Q96JD0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267875; AAK58587.1; -.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 4.5%; Score 10; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 61 SGVDPDFSGS 70
Db 57 SGVDPDFSGS 66

RESULT 11
Q91W12 PRELIMINARY; PRT; 235 AA.
ID Q91W12;
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 4.5%; Score 10; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDFSGS 70
Db 77 SGVDPDFSGS 86

RESULT 12
Q96E61 PRELIMINARY; PRT; 236 AA.
ID Q96E61;
AC Q96E61;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17259).
OS Homo sapiens (Human).

Db 57 SGVDPDFSGS 66
RESULT 10
Q96JD0 PRELIMINARY; PRT; 116 AA.
ID Q96JD0;
AC Q96JD0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267875; AAK58587.1; -.
FT NON_TER 1
FT NON_TER 116
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Query Match 4.5%; Score 10; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 61 SGVDPDFSGS 70
Db 57 SGVDPDFSGS 66

RESULT 11
Q91W12 PRELIMINARY; PRT; 235 AA.
ID Q91W12;
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 4.5%; Score 10; DB 11; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDFSGS 70
Db 77 SGVDPDFSGS 86

RESULT 12
Q96E61 PRELIMINARY; PRT; 236 AA.
ID Q96E61;
AC Q96E61;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17259).
OS Homo sapiens (Human).

Db 57 SGVDPDFSGS 66
RESULT 10
Q96JD0 PRELIMINARY; PRT; 116 AA.
ID Q96JD0;
AC Q96JD0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012876; AAH12876.1; -.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 4.5%; Score 10; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDFSGS 70
Db 77 SGVDPDFSGS 86

RESULT 13
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37;
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002035; AAH02035.1; -.
DR HSP: P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 4.5%; Score 10; DB 11; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQS 28
Db 38 ASISCRSSQS 47

RESULT 14
Q91XL0 PRELIMINARY; PRT; 211 AA.
ID Q91XL0;
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,  
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Haraoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,  
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,  
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,  
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,  
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,  
RA Tova T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
DR EMBL; AK002514; BAB22154.1; .  
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 4.1%; Score 9; DB 11; Length 211;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 QDSKDSYSTS 180  
DB 163 QDSKDSYSTS 171  
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RESULT 15  
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AC Q9R1A5;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
antibody (Mab 7, its light and heavy chains) and construction of a  
single chain antibody (scFv).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152371; AAD40242.1; .  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; Igv; 1.  
DR SMART; SM00410; Ig\_Like; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
FT NON\_TER 1  
FT NON\_TER 214 214  
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 4.1%; Score 9; DB 11; Length 214;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 QDSKDSYSTS 180  
DB 166 QDSKDSYSTS 174  
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Search completed: October 9, 2002, 19:24:57  
Job time : 18.801 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:24 ; Search time 23.5714 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPVSLPVPFGEPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1146	100.0	220	AAE12714	Human recombinant
2	1073.5	93.7	239	AA182615	Human PTHRP monocl
3	1069.5	93.3	239	AA182616	Human PTHRP monocl
4	1065.5	93.0	239	AA182617	Human PTHRP monocl
5	1058.5	92.4	239	AA182611	Human PTHRP monocl
6	1053.5	91.9	239	AA182610	Human PTHRP monocl
7	1048.5	91.5	239	AA182614	Human PTHRP monocl
8	1034.5	90.3	239	AA182612	Human PTHRP monocl
9	1034.5	90.3	239	AA182613	Human PTHRP monocl
10	1031.5	90.0	239	AA182619	Human PTHRP monocl
11	1021.5	89.1	239	AA182618	Human PTHRP monocl

12	1015.5	88.6	238	22	AA872227	Humanised 323/A3 (
13	1015.5	88.6	238	22	AA872231	Humanised 323/A3 (
14	1015.5	88.6	238	22	AA872233	Humanised 323/A3 (
15	1015.5	88.6	238	22	AA872235	Humanised 323/A3 (
16	992.5	86.6	239	18	AAW01819	Primitised anti-hu
17	992.5	86.6	239	19	AAW71876	Anti-human Fas hum
18	992.5	86.6	239	19	AAW71878	Anti-human Fas hum
19	992.5	86.6	239	19	AAW63762	Macaque primatized
20	992.5	86.6	239	21	AA812913	Anti-human Fas imm
21	992.5	86.6	239	21	AA812915	Anti-human Fas imm
22	988.5	86.3	239	19	AAW71877	Anti-human Fas hum
23	988.5	86.3	239	19	AAW71879	Anti-human Fas hum
24	988.5	86.3	239	21	AA812914	Anti-human Fas imm
25	988.5	86.3	239	21	AA812916	Anti-human Fas imm
26	987.5	86.2	238	22	AAU07744	Humanised monoclon
27	987	86.1	238	17	AA893554	Monoclonal antibod
28	986.5	86.1	238	18	AAW14942	3F4 Human IgG4 exp
29	986.5	86.1	238	18	AAW14937	Murine anti-porcine
30	978.5	85.4	238	22	AAE03754	Chimeric 2403 IgG
31	963.5	84.1	241	21	AA996303	Human IGFAM-15 imm
32	952.5	83.1	242	16	AA86323	Chimeric 6G4.2.5.1
33	952.5	83.1	242	18	AAW42323	Murine variable re
34	952.5	83.1	242	18	AAW31580	Chimeric anti IL-8
35	952.5	83.1	242	18	AAW23790	Chimeric monoclon
36	952.5	83.1	242	19	AAW69311	Anti-IL-8 mouse-hu
37	952.5	83.1	242	19	AAW40126	Chimeric Mab 6G4.2
38	952.5	83.1	242	19	AAW33745	Chimeric anti IL-8
39	952.5	83.1	242	20	AA929442	Chimeric 6G4.2.5.1
40	952.5	83.1	242	21	AA830305	Murine 6G4-2.5 ant
41	952.5	83.1	242	21	AA977748	Chimeric 6G4.2.5 a
42	929	81.1	218	22	AAE03756	Chimeric antibody
43	917	80.0	226	22	AA899376	Human interleukin
44	917	80.0	226	22	AA875009	Anti-IL8 monoclon
45	914	79.8	234	21	AA93708	The kappa chain of

#### ALIGNMENTS

```

RESULT 1
AAE12714
ID  AAE12714 standard; Protein; 220 AA.
XX
AC  AAE12714;
XX
DT  04-JAN-2002 (first entry)
XX
DE  Human recombinant immunoglobulin (Ig) light chain region.
XX
KW  Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
KW  light chain region; cancer; breast; ovary; lung; bladder;
KW  cytostatic; therapy; immunoglobulin; Ig.
XX
OS  Homo sapiens.
XX
PN  WO200175110-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US10589.
XX
PR  30-MAR-2000; 2000US-0538913.
XX
PA  (DYAX-) DYAX CORP.
XX
PI  Hoogenboom HRJM, Henderikx MPG;
XX
DR  WPI; 2001-626437/72.
XX
N-PSDB; RAD20744.
XX
PT  Novel isolated tumor-associated antigen mucin-1-specific binding member
PT  for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT  its portion for binding to an epitope of the protein core of mucin-1

```





Db 200 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 5

AA82611  
ID AAY82611 standard; Protein; 239 AA.

XX AC AAY82611;  
XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX DR N-PSDB; AAA13921.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
XX including metastasis, and pain

XX PS Claim 31; Page 34-35; 88pp; Japanese.

XX CC The present invention describes a human monoclonal antibody to  
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
XX its fragments, following the stimulation of PTHrP has the following  
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
XX the release of calcium from bone; or (c) inhibits elevation of blood  
XX calcium content. The monoclonal antibody can be used in the treatment  
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome  
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
XX antiinflammatory activities. The present sequence represents a  
XX human PTHrP monoclonal antibody clone protein sequence from the  
XX present invention.

XX SQ Sequence 239 AA;

Query Match 92.4%; Score 1058.5; DB 21; Length 239;

Best Local Similarity 92.7%; Pred. No. 2.3e-64;

Matches 204; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIVLTQSPSLPVTGPEPATISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLYSGSHRA 60

Db 21 DIVMTQSPSLPVTGPEPATISCRSSQSLHNSGNNYLDWFLQKPGQSPQLLYLGSNRA 80

Qy 61 SGVDPDRFSGVSGTDFTLIRSRVEAEDGVGYCYMQGLQSPFTFGPGTKVDIKRGTVAAPS 120

Db 81 SGVDPDRFSGVSGTDFTLKLSRVEAEDGVGYCYMQALQIPFTFGPGTKVDIKR-TVAAPS 139

Qy 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180

Db 140 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 199

QY 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

Db 200 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 6

AA82610  
ID AAY82610 standard; Protein; 239 AA.

XX AC AAY82610;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 164 /label= Phe, Ser, Tyr, Cys

FT /label= Phe, Leu

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX DR N-PSDB; AAA13920.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
XX including metastasis, and pain

XX PS Claim 31; Page 33; 88pp; Japanese.

XX CC The present invention describes a human monoclonal antibody to  
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
XX its fragments, following the stimulation of PTHrP has the following  
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
XX the release of calcium from bone; or (c) inhibits elevation of blood  
XX calcium content. The monoclonal antibody can be used in the treatment  
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome  
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
XX antiinflammatory activities. The present sequence represents a  
XX human PTHrP monoclonal antibody clone protein sequence from the  
XX present invention.

XX SQ Sequence 239 AA;

Query Match 91.9%; Score 1053.5; DB 21; Length 239;

Best Local Similarity 92.7%; Pred. No. 5e-64;

Matches 204; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPATISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLYSGSHRA 60

Db 21 DIVMTQSPSLPVTGPEPATISCRSSQSLHNSGNNYLDWFLQKPGQSPQLLYLGSNRA 80

Db 21 DIVMTQXPLSLPVTGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 80  
 Qy 61 SGVPDRFSGSGVSGDTFTLRISRVAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
 Db 81 SGVPDRFSGSGVSGDTFTLRISRVAEADVGYVYCMQGLQSPFTFGPGTKVDIKR-TVAAPS 139  
 Qy 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180  
 Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199  
 Qy 181 LSSLTLSKADYEHKKYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 200 LSSLTLSKADYEHKKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7  
 AAY82614  
 ID AAY82614 standard; Protein; 239 AA.  
 XX  
 AC AAY82614;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 117 /label= Leu, Ile, Val  
 FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 216 /note= "possible Val"  
 FT  
 XX JP2000080100-A.  
 XX  
 XX PD 21-MAR-2000.  
 XX  
 XX PF 12-OCT-1998; 98JP-0304793.  
 XX  
 XX PR 17-JUN-1998; 98JP-0188196.  
 XX PR 26-JUN-1998; 98JP-0196729.  
 XX  
 XX PA (NISR ) JAPAN TOBACCO INC.  
 XX  
 XX DR WPI; 2000-286723/25.  
 XX DR N-PSDB; AAA13924.  
 XX  
 XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
 XX PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 XX PT including metastasis, and pain  
 XX  
 XX PS Claim 31; Page 43; 88pp; Japanese.  
 XX  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal

CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 91.5%; Score 1048.5; DB 21; Length 239;  
 Best Local Similarity 92.3%; Pred. No. 1.1e-63;  
 Matches 203; Conservative 4; Mismatches 12; Indels 1; Gaps 1;  
 Qy 1 EIVLTQSLPLSLPVTGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 60  
 Db 21 DIVMTQXPLSLPVTGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 80  
 Qy 61 SGVPDRFSGSGVSGDTFTLRISRVAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
 Db 81 SGVPDRFSGSGVSGDTFTLRISRVAEADVGYVYCMQGLQSPFTFGPGTKVDIKR-TVAAPS 139  
 Qy 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180  
 Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199  
 Qy 181 LSSLTLSKADYEHKKYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 200 LSSLTLSKADYEHKKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8  
 AAY82612  
 ID AAY82612 standard; Protein; 239 AA.  
 XX  
 AC AAY82612;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 1B3-9-16 protein SEQ ID NO:8.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 84 /note= "possibly Pro"  
 FT  
 XX JP2000080100-A.  
 XX  
 XX PD 21-MAR-2000.  
 XX  
 XX PF 12-OCT-1998; 98JP-0304793.  
 XX  
 XX PR 17-JUN-1998; 98JP-0188196.  
 XX PR 26-JUN-1998; 98JP-0196729.  
 XX  
 XX PA (NISR ) JAPAN TOBACCO INC.  
 XX  
 XX DR WPI; 2000-286723/25.  
 XX DR N-PSDB; AAA13922.  
 XX  
 XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
 XX PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 XX PT including metastasis, and pain

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PS Claim 31; Page 37-38; 88pp; Japanese.
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
SQ Sequence 239 AA;

Query Match 90.3%; Score 1034.5; DB 21; Length 239;
Best Local Similarity 91.8%; Pred. No. 9.6e-63;
Matches 202; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYSGSHRA 60
DB :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 DIVMXQXPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYLGXNRA 80
QY 61 SGVDPDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 SGVXDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 139
QY 121 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
QY 181 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9
AA82613
ID AA82613 standard; Protein: 239 AA.
XX
AC AA82613;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 1B4-10-13 protein SEQ ID NO:10.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 77 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 84 /label= "possibly Pro"
FT Misc-difference 117 /label= Leu, Ile, Val
XX
PN JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0185196.
XX
XX 26-JUN-1998; 98JP-0196729.

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PS Claim 31; Page 37-38; 88pp; Japanese.
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
SQ Sequence 239 AA;

Query Match 90.3%; Score 1034.5; DB 21; Length 239;
Best Local Similarity 91.8%; Pred. No. 9.6e-63;
Matches 202; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYSGSHRA 60
DB :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 DIVMXQXPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYLGXNRA 80
QY 61 SGVDPDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 SGVXDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 139
QY 121 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
QY 181 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9
AA82613
ID AA82613 standard; Protein: 239 AA.
XX
AC AA82613;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 1B4-10-13 protein SEQ ID NO:10.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 77 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 84 /label= "possibly Pro"
FT Misc-difference 117 /label= Leu, Ile, Val
XX
PN JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0185196.
XX
XX 26-JUN-1998; 98JP-0196729.

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XX (NISB ) JAPAN TOBACCO INC.
XX WPI; 2000-286723/25.
DR N-PSDB; AAA13923.
XX A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX Claim 31; Page 40; 88pp; Japanese.
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of teeth, periodontal
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
SQ Sequence 239 AA;

Query Match 90.3%; Score 1034.5; DB 21; Length 239;
Best Local Similarity 91.8%; Pred. No. 9.6e-63;
Matches 202; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYSGSHRA 60
DB :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 DIVMTQSPLSLPTPGEPASISCRSSQLHNSNGYTYLDWYLKQKQSPQLLIYLGXNRA 80
QY 61 SGVDPDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 SGVXDRFSGSGVGTFTLRISRYEAEADVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 139
QY 121 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 VFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
QY 181 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 10
AA82619
ID AA82619 standard; Protein: 239 AA.
XX
AC AA82619;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:22.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "possibly Met"
FT Misc-difference 3 /label= Phe, Leu, Ile, Val
FT Misc-difference 4

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Qy	181	LSSTLTLSKADYEKKHYACAEVTHOGLSSPYKSFNKGEC	220
Db	200	LSSTLTLSKADYEKKHYACAEVTHOGLSSPYKSFNKGEC	239
	RESULT 11		
	AA82618		
ID	AA82618	standard; Protein; 239 AA.	
XX	AC		
XX	AC	AA82618;	
XX	DT	02-AUG-2000	(first entry)
XX	DE	Human PTHrP monoclonal antibody clone 4B4-6-21	pro
XX	DE	Human PTHrP monoclonal antibody clone 4B4-6-21	pro
XX	KW	Human; parathyroid hormone related protein; PTHrP	
KW	KW	hypercalcaemia; rheumatoid arthritis; bone cancer	
KW	KW	fracture; cachexia; tooth disease; periodontal di	
KW	KW	sepsis; systemic inflammatory response syndrome;	
KW	KW	hypophosphataemia; antiarthritic; cytostatic; ant	
XX	OS	Homo sapiens.	
XX	XX		
XX	Key	Location/Qualifiers	
FT	FT	Misc-difference 25	
FT	FT	/label= Ile, Thr, Asn, Ser	
FT	FT	Misc-difference 27	
FT	FT	/label= Phe, Ser, Tyr, Cys	
FT	FT	Misc-difference 213	
FT	FT	/label= Gln, Lys, Glu	
FT	FT	Misc-difference 215	
FT	FT	/label= Gln, Lys, Glu	
FT	FT	Misc-difference 219	
FT	FT	/label= Cys, Trp	
FT	FT	Misc-difference 220	
FT	FT	/label= Val, Ala, Glu, Gly	
FT	FT	Misc-difference 222	
FT	FT	/label= Ile, Thr, Asn, Ser	
XX	XX		
XX	PN	JP2000080100-A.	
XX	XX		
XX	PD	21-MAR-2000.	
XX	PF	12-OCT-1998; 98JP-0304793.	
XX	XX		
XX	PR	17-JUN-1998; 98JP-0188196.	
XX	PR	26-JUN-1998; 98JP-0196729.	
XX	XX		
XX	PA	(NISR ) JAPAN TOBACCO INC.	
XX	PA		
XX	WI	WI: 2000-286723/25.	
XX	DR	N-PSDB; AA813928.	
XX	XX		
XX	PT	A human monoclonal antibody to parathyroid hormone	
XX	PT	useful for treating hypercalcaemia, rheumatoid art	
XX	PT	including metastasis, and pain	
XX	PS	Claim 31; Page 55; 88pp; Japanese.	
XX	XX		
XX	CC	The present invention describes a human monoclonal	
XX	CC	parathyroid hormone related protein (PTHrP). The	
XX	CC	its fragments, following the stimulation of PTHrP	
XX	CC	properties: (a) inhibits intracellular elevation	
XX	CC	the release of calcium from bone; or (c) inhibits	
XX	CC	calcium content. The monoclonal antibody can be u	
XX	CC	of hypercalcaemia, rheumatoid arthritis, cancer o	
XX	CC	metastasis, pain, fracture, cachexia, diseases o	
XX	CC	diseases and gingiva, sepsis, systemic inflamat	
XX	CC	(SIRS) and hypophosphataemia. It has antiarthrit	
XX	CC	antitumour activities. The present sequence	
XX	CC	human PTHrP monoclonal antibody clone protein seq	
XX	CC	present invention.	

XX SQ Sequence 239 AA;  
 Query Match 89.1%; Score 1021.5; DB 21; Length 239;  
 Best Local Similarity 90.0%; Pred. No. 7.3e-62;  
 Matches 198; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPVSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60  
 DB 21 DIVMQXPLSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 80  
 QY 61 SGVPDRFSGVSGTDTFTLRISRVAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 120  
 DB 81 SGVPDRFSGVSGTDTFTLRISRVAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 139  
 QY 121 VFIPTPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDNDKSTYS 180  
 DB 140 VFIPTPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDNDKSTYS 199  
 QY 181 LSSTLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 200 LSSTLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12  
 AAB72227  
 ID AAB72227 standard; Protein: 238 AA.  
 XX AAB72227;  
 AC AAB72227;  
 XX AAB72227;  
 DT 10-MAY-2001 (first entry)  
 XX Humanised 323/A3 (IgG1) antibody light chain amino acid sequence.  
 DE Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;  
 KW light chain.  
 XX Mus sp.  
 OS Homo sapiens.  
 XX WO200107082-A1.  
 XX 01-FEB-2001.  
 XX 23-JUL-1999; 99WO-EP05271.  
 XX 23-JUL-1999; 99WO-EP05271.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Knick VC, Stimmel JB, Thurmond LM;  
 XX WPI; 2001-182729/18.  
 DR N-PSDB; AAF63373.  
 XX Combination for treating cancer (e.g. breast, gastric or prostate  
 PT cancers), or in the manufacture of a medicament for anti-cancer  
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody  
 PT with a chemotherapeutic agent -  
 XX Disclosure: Fig 15; 103pp; English.  
 XX This invention relates to a combination of an anti-Ep-CAM (cyclic  
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA  
 CC replication. The antibody exhibits cytostatic activity and is useful in  
 CC the manufacture of a medicament for use in anti-cancer therapy,  
 CC characterised in that a chemotherapeutic agent, which is capable of  
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is  
 CC co-administered to a patient with an anti-Ep-CAM antibody. The  
 CC combination is useful for treating cancer, particularly colorectal

CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell  
 CC lung cancer. The present sequence represents the light chain of  
 CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used  
 CC in the combination of the invention.  
 XX Sequence 238 AA;  
 SQ Query Match 88.6%; Score 1015.5; DB 22; Length 238;  
 Best Local Similarity 90.5%; Pred. No. 1.8e-61;  
 Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPVSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60  
 DB 20 DIVMTQSPVSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 79  
 QY 61 SGVPDRFSGVSGTDTFTLRISRVAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 120  
 DB 80 SGVPDRFSGVSGTDTFTLRISRVAEADVGVYCMQGLQSPFTFGPTKVDIKRGTVAAAPS 138  
 QY 121 VFIPTPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDNDKSTYS 180  
 DB 139 VFIPTPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDNDKSTYS 198  
 QY 181 LSSTLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 199 LSSTLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 13  
 AAB72231  
 ID AAB72231 standard; Protein: 238 AA.  
 XX AAB72231;  
 AC AAB72231;  
 XX AAB72231;  
 DT 10-MAY-2001 (first entry)  
 XX Humanised 323/A3 (IgG1) antibody kappa light chain amino acid sequence.  
 DE Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
 KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;  
 KW light chain.  
 XX Mus sp.  
 OS Homo sapiens.  
 XX WO200107082-A1.  
 XX 01-FEB-2001.  
 XX 23-JUL-1999; 99WO-EP05271.  
 XX 23-JUL-1999; 99WO-EP05271.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Knick VC, Stimmel JB, Thurmond LM;  
 XX WPI; 2001-182729/18.  
 XX Combination for treating cancer (e.g. breast, gastric or prostate  
 PT cancers), or in the manufacture of a medicament for anti-cancer  
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody  
 PT with a chemotherapeutic agent -  
 XX Example 3; Fig 6; 103pp; English.  
 XX This invention relates to a combination of an anti-Ep-CAM (cyclic  
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA  
 CC replication. The antibody exhibits cytostatic activity and is useful in  
 CC the manufacture of a medicament for use in anti-cancer therapy,  
 CC characterised in that a chemotherapeutic agent, which is capable of



adenosine monophosphate) antibody with a chemotherapeutic agent, that is capable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (M) of cell enlargement (G2)/DNA replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-administered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell lung cancer. The present sequence represents the kappa light chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be used in the combination of the invention.

CC	XX	SQ	Sequence	238	AA;
CC	Query Match		88.6%;	Score	1015.5; DB 22; Length 238;
CC	Best Local Similarity		90.5%;	Pred. No.	1.8e-61;
CC	Matches 199;	Conservative	8;	Mismatches	12; Indels 1; Gaps 1;
QY	1	EIVLTQSP	LSLPVTGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA	60	
DB	20	DIVMTQSP	LSLPVTGEPASISCRSKNLLHNSGITLYLWYLQKPGQSPQLLIYQMSNLA	79	
QY	61	SGVPRFSG	SVSGTDFTLRISRVEAEDVGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS	120	
DB	80	SGVPRFSS	SGSGTDFTLKISRVEAEDVGVVYCAQNLEIPRTFGGQTKVEIKR-TVAAPS	138	
QY	121	VFIFPPSD	QLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDS	180	
DB	139	VFIFPPSD	QLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDS	198	
QY	181	LSSTLTLS	KADYKHKVYACEVTHOGLSPYTKSFNRGEC	220	
DB	199	LSSTLTLS	KADYKHKVYACEVTHOGLSPYTKSFNRGEC	238	

Search completed: October 9, 2002, 19:10:28  
Job time : 24.5714 secs

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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:09:15 ; Search time 8.97959 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPVLPVTPGPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCFUS-COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	992.5	86.6	239	3	US-08-487-550-6
2	952.5	83.1	242	1	US-08-398-613A-56
3	952.5	83.1	242	1	US-08-398-612A-56
4	952.5	83.1	242	1	US-08-398-611A-56
5	952.5	83.1	242	2	US-08-491-334A-56
6	952.5	83.1	242	3	US-09-027-449-42
7	952.5	83.1	242	3	US-08-804-444A-42
8	952.5	83.1	242	4	US-09-026-985-42
9	893.5	78.0	219	3	US-09-027-449-72
10	893.5	78.0	219	3	US-09-026-985-72
11	893.5	78.0	242	3	US-09-027-449-51
12	893.5	78.0	242	3	US-09-027-449-56
13	893.5	78.0	242	3	US-09-027-449-62
14	893.5	78.0	242	3	US-08-804-444A-51
15	893.5	78.0	242	3	US-08-804-444A-56
16	893.5	78.0	242	4	US-09-026-985-51
17	893.5	78.0	242	4	US-09-026-985-62
18	893.5	78.0	242	4	US-08-952-235-1
19	889	77.6	220	4	US-07-916-098A-56
20	881.5	76.9	241	2	US-09-247-352-4
21	876	76.4	214	4	US-08-480-753-8
22	876	76.4	215	2	US-08-887-352B-13
23	872	76.1	218	3	US-08-466-151-9
24	872	76.1	218	4	US-09-109-207C-13
25	872	76.1	218	4	US-09-296-005-13
26	872	76.1	218	4	US-08-466-163B-9
27	872	76.1	218	4	US-08-466-163B-9

28	870.5	76.0	214	2	US-08-480-753-6
29	870.5	76.0	214	3	US-09-041-889-11
30	870.5	76.0	214	3	US-08-837-058-11
31	865	75.5	218	2	US-08-887-352B-15
32	865	75.5	218	2	US-08-887-352B-17
33	865	75.5	218	2	US-08-887-352B-19
34	865	75.5	218	2	US-08-887-352B-24
35	865	75.5	218	4	US-09-109-207C-15
36	865	75.5	218	4	US-09-109-207C-17
37	865	75.5	218	4	US-09-109-207C-19
38	865	75.5	218	4	US-09-109-207C-24
39	865	75.5	218	4	US-09-296-005-15
40	865	75.5	218	4	US-09-296-005-17
41	865	75.5	218	4	US-09-296-005-19
42	865	75.5	218	4	US-09-296-005-24
43	863	75.3	218	4	US-09-282-505-1
44	863	75.3	218	4	US-09-054-255-1
45	863	75.3	218	5	PCT-US96-13152-2

ALIGNMENTS

RESULT 1  
US-08-487-550-6  
; Sequence 6, Application US/08487550  
; Patent No. 6113898

GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/487,550

APPLICATION NUMBER: 07-JUN-1995

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-550-6

Query Match 86.6%; Score 992.5; DB 3; Length 239;

Best Local Similarity 87.7%; Pred. No. 7.9e-81;

Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPVLPVTPGPASISCRSSQLHNSNGYLYLDWYLOKPGSPOLLVYSGHRA 60

Db 21 EVVMTQSPVLPVTPGPASISCRSSQLKHNSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80

Qy 61 SGVPDRFSGSVSGTDTLRLISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 81 SGVPDRFSGSVSGTDTLRLISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 139  
Qy 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
Qy 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239  
RESULT 2  
US-08-398-613A-56  
; Sequence 56, Application US/08398613A  
; Patent No. 5677426  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398, 613A  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 874P1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1489  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-398-613A-56  
Query Match 83.1%; Score 952.5; DB 1; Length 242;  
Best Local Similarity 84.1%; Pred. No. 2.9e-77;  
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPLSPLVPTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 24 DIVMTQTPLSLPSVLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVSGTDTLRLISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 84 SGVPDRFSGSVSGTDTLRLISRVEAEDGLVFCQSOSTHVPLTFGAGTKLEKR-AVAAPT 142  
Qy 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 143 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 202

Qy 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 203 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 242  
RESULT 3  
US-08-398-612A-56  
; Sequence 56, Application US/08398612A  
; Patent No. 5686070  
; GENERAL INFORMATION:  
; APPLICANT: Doershuk, Claire M.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398, 612A  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398611  
; FILING DATE: 01-MAR-1995  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-398-612A-56  
Query Match 83.1%; Score 952.5; DB 1; Length 242;  
Best Local Similarity 84.1%; Pred. No. 2.9e-77;  
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPLSPLVPTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 24 DIVMTQTPLSLPSVLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVSGTDTLRLISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 84 SGVPDRFSGSVSGTDTLRLISRVEAEDGLVFCQSOSTHVPLTFGAGTKLEKR-AVAAPT 142  
Qy 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 143 VFIFPPSDEQLKSGTASVVCVLLNNFYPRACKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 202  
Qy 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220

Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

## RESULT 4

US-08-398-611A-56  
; Sequence 56, Application US/08398611A  
; Patent No. 5702946  
; GENERAL INFORMATION:  
; APPLICANT: Doershuk, Claire M.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment  
; TITLE OF INVENTION: Of Inflammatory Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,611A  
; FILING DATE: 01-Mar-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-Mar-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-398-611A-56

Query Match 83.1%; Score 952.5; DB 1; Length 242;

Best Local Similarity 84.1%; Pred. No. 2.9e-77;

Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 24 DIVMTQTPLSLPVSLGDAQSISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNR 83

QY 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTPGCTKVDIKRGTVAA 120

Db 84 SGVPDRFSGSVSGDTFTLRISRVEAEDGLGYFCQSQTHTVPLTFGAGTKLELKR-A 142

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 180

Db 143 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 202

QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

## RESULT 5

US-08-491-334A-56

; Sequence 56, Application US/08491334A  
; Patent No. 5874080  
; GENERAL INFORMATION:  
; APPLICANT: Hebert, Caroline A.  
; APPLICANT: Kabakoff, Rhona C.  
; APPLICANT: Moore, Mark W.  
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory  
; TITLE OF INVENTION: Disorders and Asthma  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,334A  
; FILING DATE: 27-Jun-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398611  
; FILING DATE: 01-Mar-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-Mar-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-491-334A-56

Query Match 83.1%; Score 952.5; DB 2; Length 242;

Best Local Similarity 84.1%; Pred. No. 2.9e-77;

Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60

Db 24 DIVMTQTPLSLPVSLGDAQSISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNR 83

QY 61 SGVPDRFSGSVSGDTFTLRISRVEAEDGVVYCMQGLQSPFTPGCTKVDIKRGTVAA 120

Db 84 SGVPDRFSGSVSGDTFTLRISRVEAEDGLGYFCQSQTHTVPLTFGAGTKLELKR-A 142

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 180

Db 143 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 202

QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

## RESULT 6

US-09-027-449-42

; Sequence 42, Application US/09027449

; Patent No. 6025158

; GENERAL INFORMATION:

; APPLICANT: Gonzalez, Tania R.





;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/026,985  
;; FILING DATE: 20-Feb-1998  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Love, Richard B.  
;; REGISTRATION NUMBER: 34,659  
;; REFERENCE/DOCKET NUMBER: P1085R3-1  
;; TELEPHONE: 650/225-5530  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-09-026-985-42

Query Match 83.1%; Score 952.5; DB 4; Length 242;  
Best Local Similarity 84.1%; Pred. No. 2.9e-77;  
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;  
QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60  
Db 24 DIVMTQPLSLPVSLGDOASISCRSSQSLVHGIGNTYLYLHWYLOKPGQSPKLLIYKYSNRF 83  
QY 61 SGVPRFSGSGTGDTFLIRISRAEDVGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db 84 SGVPRFSGSGTGDTFLIRISRAEDVGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPT 142  
QY 121 VFIFPPSEQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 180  
Db 143 VFIFPPSEQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 202  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 9  
US-09-027-449-72  
; Sequence 72, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:

;;  
;; NAME: Love, Richard B.  
;; REGISTRATION NUMBER: 34,659  
;; REFERENCE/DOCKET NUMBER: P1085R3-2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-5530  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 72:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 219 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-09-027-449-72

Query Match 78.0%; Score 893.5; DB 3; Length 219;  
Best Local Similarity 79.5%; Pred. No. 4.4e-72;  
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
QY 1 EIVLTQSLPLVPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIIYSGSHRA 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYLYHWYQKPKAPKLLIYKYSNRF 60  
QY 61 SGVPRFSGSGTGDTFLIRISRAEDVGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db 61 SGVPRFSGSGTGDTFLIRISRAEDVGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 119  
QY 121 VFIFPPSEQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 180  
Db 120 VFIFPPSEQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYS 179  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 180 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 10  
US-09-026-985-72  
; Sequence 72, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

## US-09-026-985-72

Query Match 78.0%; Score 893.5; DB 4; Length 219;  
Best Local Similarity 79.5%; Pred. No. 4.4e-72;  
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
  
Qy 1 EIVLTQSPFLSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPOLLIIYSGSHRA 60  
Db 1 DIQMTQSPSSLSASVGDRTVITTCRSSQSLVHGIGATYLHWYQKPGKAPKLLIYKVS NRF 60  
  
Qy 61 SGVPDRFSGSVSGTDTFLTRISVEAEDGVYVCMGLOQSPFTFGPTGKVDIKRGTVAAPS 120  
Db 61 SGVPSRFSGSGGTDTFTLTISSLPQEDFATYYCSQSTHVPLTFGQGTKEIKR-TVAAPS 119  
  
Qy 121 VFIPFSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYS 180  
Db 120 VFIPFSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYS 179  
  
Qy 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 180 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 219

## RESULT 11

US-09-027-449-51  
; Sequence 51, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027.449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; APPLICATION DATA:  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; Query Match 78.0%; Score 893.5; DB 3; Length 242;  
; Best Local Similarity 79.5%; Pred. No. 4.9e-72;  
; Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
US-09-027-449-51

Qy 1 EIVLTQSPFLSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPOLLIIYSGSHRA 60  
Db 24 DIQMTQSPSSLSASVGDRTVITTCRSSQSLVHGIGATYLHWYQKPGKAPKLLIYKVS NRF 83  
  
Qy 61 SGVPDRFSGSVSGTDTFLTRISVEAEDGVYVCMGLOQSPFTFGPTGKVDIKRGTVAAPS 120  
Db 84 SGVPSRFSGSGGTDTFTLTISSLPQEDFATYYCSQSTHVPLTFGQGTKEIKR-TVAAPS 142  
  
Qy 121 VFIPFSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYS 180  
Db 143 VFIPFSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSSTYS 202  
  
Qy 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 203 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 242

## RESULT 12

US-09-027-449-56  
; Sequence 56, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027.449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; APPLICATION DATA:  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-027-449-56  
; Query Match 78.0%; Score 893.5; DB 3; Length 242;  
; Best Local Similarity 79.5%; Pred. No. 4.9e-72;  
; Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
US-09-027-449-56

Qy 1 EIVLTQSPFLSLPVTGPEPASISCRSSQSLHNSGYTYLDWLQKPGQSPOLLIIYSGSHRA 60  
Db 24 DIQMTQSPSSLSASVGDRTVITTCRSSQSLVHGIGATYLHWYQKPGKAPKLLIYKVS NRF 83

QY	61	SGVPDRSGSVSGTDTFLRLSRVEAEADVGYVYCMQGLQSPFFPGPCTKYVDIKRGTVAAAPS	120
Db	84	SGVPRFSGSGSGGDFLLTILSSQLQPEDFATYICQSTHVTPLTFGTQGTKEIKR-TVAAAPS	142
QY	121	VFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS	180
Db	143	VFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS	202
QY	181	LSSTLTLSKADYEKHKYIACEVTHQGLSSPVTKSFNRGEC	220
Db	203	LSSTLTLSKADYEKHKYIACEVTHQGLSSPVTKSFNRGEC	242

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RESULT 13
US-09-027-449-62
; Sequence 62, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-62

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Db      143  VFIFPPDEQLKSGTASVWCLLNFPYREAKVQWKVDNALQSGNSQSEVTEQDSKDTYS 202
Qy      181  LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 220
Db      203  LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 14
US-08-804-444A-51
: Sequence 51 Application US/0880444A

```

RESULT 14  
US-08-804-444A-51  
; Sequence 51, Application US/08804444A  
; Patent No. 6117980  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania N  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,444A  
; FILING DATE: 21-Feb-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-804-444A-51

RESULT 15  
US-08-804-444A-56  
; Sequence 56, Application US/08804444A  
; Patent No. 6117980

GENERAL INFORMATION:  
APPLICANT: Gonzalez, Tania N  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,444A  
FILING DATE: 21-Feb-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-804-444A-56

Query Match 78.0%; Score 893.5; DB 3; Length 242;  
Best Local Similarity 79.5%; Pred. No. 4.9e-72;  
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
Db 24 DIQMTQSPSSLSASVGDRTITCRSSQSLVHGIGATYLVHWYQQKPKAPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVSGTDFTLIRISRVAEADVGVVYCMQGLQSPFTFGPTKVDIKRGTVAA 120  
Db 84 SGVPSRFSGSGSGTDFTLTISSLQPEDFATYVCQSQTHVPLTFGQGTKEIKR-TVA 142  
Qy 121 VFIPPPDEQLKSGTASVYVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 180  
Db 143 VFIPPPDEQLKSGTASVYVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSK 202  
Qy 181 LSSLTILTSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
Db 203 LSSLTILTSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 242

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Job time : 8.97959 secs

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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:10:35 ; Search time 86.7092 Seconds  
(without alignments)  
893.051 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 1146  
Sequence: 1 EIVLTQSLPLVTPGEPAS.....EVTHQGLSPVTKSFNRGRC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
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- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.\*
- 25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1146	100.0	220	US-09-822-698A-24
2	1052.5	91.8	219	Sequence 24, Appl
3	1050.5	91.7	239	Sequence 104, App
4	1050.5	91.7	239	Sequence 8, Appl
5	1050.5	91.7	239	Sequence 8, Appl
6	1050.5	91.7	239	Sequence 8, Appl
7	1050.5	91.7	239	Sequence 8, Appl

8	1023.5	89.3	219	23	US-09-972-656-94	Sequence 94, Appl
9	1016.5	88.7	219	23	US-09-972-656-106	Sequence 106, Appl
10	992.5	86.6	239	14	US-09-046-351-78	Sequence 78, Appl
11	992.5	86.6	239	14	US-09-046-351-82	Sequence 82, Appl
12	992.5	86.6	239	17	US-09-383-916-6	Sequence 6, Appl
13	992.5	86.6	239	19	US-09-576-424-6	Sequence 8, Appl
14	988.5	86.3	239	14	US-09-046-351-80	Sequence 6, Appl
15	988.5	86.3	239	14	US-09-046-351-84	Sequence 8, Appl
16	986.5	86.1	238	11	US-08-721-612B-19	Sequence 19, Appl
17	986.5	86.1	238	11	US-08-721-612C-19	Sequence 19, Appl
18	978.5	85.4	238	20	US-09-698-705-10	Sequence 10, Appl
19	976.5	85.2	262	21	US-09-760-479-658	Sequence 658, App
20	971	84.7	228	23	US-09-909-567-50	Sequence 50, Appl
21	969.5	84.6	219	23	US-09-972-656-92	Sequence 92, Appl
22	966.5	84.3	244	21	US-09-760-479-641	Sequence 641, App
23	963.5	84.1	241	26	US-60-128-194-1	Sequence 1, Appl
24	952.5	83.1	242	7	US-08-398-614A-56	Sequence 56, Appl
25	952.5	83.1	242	7	US-08-398-614A-56	Sequence 56, Appl
26	952.5	83.1	242	12	US-08-804-444-56	Sequence 56, Appl
27	952.5	83.1	242	14	US-09-012-116-42	Sequence 42, Appl
28	952.5	83.1	242	15	US-09-121-952A-42	Sequence 42, Appl
29	952.5	83.1	242	15	US-09-122-513A-42	Sequence 42, Appl
30	952.5	83.1	242	16	US-09-234-182A-42	Sequence 42, Appl
31	952.5	83.1	242	16	US-09-234-340A-42	Sequence 42, Appl
32	952.5	83.1	242	18	US-09-489-394-42	Sequence 42, Appl
33	952.5	83.1	242	21	US-09-726-258-42	Sequence 42, Appl
34	929	81.1	218	20	US-09-698-705-12	Sequence 12, Appl
35	917	80.0	226	1	PCT-US00-27237-38	Sequence 38, Appl
36	917	80.0	226	1	PCT-US00-33042-38	Sequence 38, Appl
37	917	80.0	226	18	US-09-453-234-38	Sequence 38, Appl
38	917	80.0	226	18	US-09-456-090-38	Sequence 38, Appl
39	917	80.0	226	18	US-09-456-090A-38	Sequence 38, Appl
40	914	79.8	234	18	US-09-472-087-17	Sequence 17, Appl
41	914	79.8	234	18	US-09-472-087-69	Sequence 69, Appl
42	908	79.2	224	1	PCT-US00-27237-44	Sequence 44, Appl
43	908	79.2	224	1	PCT-US00-27237-78	Sequence 78, Appl
44	908	79.2	224	1	PCT-US00-33042-44	Sequence 44, Appl
45	908	79.2	224	1	PCT-US00-33042-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1  
US-09-822-698A-24  
; Sequence 24, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hooqenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 24  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1  
US-09-822-698A-24

Query Match	100.0%;	Score 1146;	DB 22;	Length 220;
Best Local Similarity	100.0%;	Pred. No. 4.1e-94;		
Matches	220;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	EIVLTQSLPLVTPGEPAS	1	SCRSSQSLLSHNGYTLDWYLRKPGSPQLLYSGSHRA 60
Db	1	EIVLTQSLPLVTPGEPAS	1	SCRSSQSLLSHNGYTLDWYLRKPGSPQLLYSGSHRA 60

QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
QY 121 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 121 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 2  
US-09-972-656-104  
; Sequence 104, Application US/09972656  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 104  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-104

Query Match 91.8%; Score 1052.5; DB 23; Length 219;  
Best Local Similarity 93.2%; Pred. No. 9.7e-86;  
Matches 205; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 60  
Db 1 EIVLTQSPSLPLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 60  
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 119  
QY 121 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 120 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 179  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 180 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 3  
US-09-924-340-8  
; Sequence 8, Application US/09924340  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephanie  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent

; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-924-340-8  
Query Match 91.7%; Score 1050.5; DB 23; Length 239;  
Best Local Similarity 92.7%; Pred. No. 1.6e-85;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 60  
Db 21 DIVMTQSPFLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 80  
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 81 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 139  
QY 121 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 140 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4  
US-09-994-590-8  
; Sequence 8, Application US/09994590  
; GENERAL INFORMATION:  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US3.DIV  
; CURRENT APPLICATION NUMBER: US/09/994,590  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-994-590-8

Query Match 91.7%; Score 1050.5; DB 23; Length 239;  
Best Local Similarity 92.7%; Pred. No. 1.6e-85;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 60  
Db 21 DIVMTQSPFLPVTGPGPASPISCRSSOSLLHNGYTYLDWYLOKPGSPOLLIIYSGSHRA 80  
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120

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Db 81 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 239

RESULT 5
US-10-000-489-8
; Sequence 8, Application US/10000489
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-10-000-489-8

Query Match 91.7%; Score 1050.5; DB 24; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLFPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 80
Qy 61 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
Db 81 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 239

RESULT 6
US-10-000-986-8
; Sequence 8, Application US/10000986
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US9.DIV
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; CURRENT APPLICATION NUMBER: US/10/000,986
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-10-000-986-8

Query Match 91.7%; Score 1050.5; DB 24; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLFPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 80
Qy 61 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
Db 81 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACVETHQGLSSPVTKSFNRGEC 239

RESULT 7
US-60-305-456-8
; Sequence 8, Application US/60305456
; GENERAL INFORMATION:
; APPLICANT: BEJANIN, Stephane
; APPLICANT: TANAKA, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
; FILE REFERENCE: 97.US5.PRO
; CURRENT APPLICATION NUMBER: US/60/305,456
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-305-456-8

Query Match 91.7%; Score 1050.5; DB 26; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLFPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 80
Qy 61 SGVPDRFSGSGGDTFLTKISRVEAEDGVVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
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; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-94

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> CURRENT APPLICATION NUMBER: 09/027,047/3538
> CURRENT FILING DATE: 1998-03-23
> EARLIER APPLICATION NUMBER: JP HEI 9-67938
> EARLIER FILING DATE: 1997-03-21
> NUMBER OF SEQ ID NOS: 189
> SOFTWARE: PatentIn Ver. 2.0
> SEQ ID NO 78
> LENGTH: 239
> TYPE: PRT
> ORGANISM: Artificial Sequence
> FEATURE:
> OTHER INFORMATION: Description of Artificial Sequence: L chain of a
> OTHER INFORMATION: humanized anti-Fas antibody
> JS-09-046-351-78

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> SOURCE: 054-EP NO. 1.1
> SOFTWARE: PatentIn Ver. 2.0
> SEQ ID NO 78
> LENGTH: 239
> TYPE: PRT
> ORGANISM: Artificial Sequence
> FEATURE:
> OTHER INFORMATION: Description of Artificial Sequence: L chain of a
> OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-78

Query Match      86.6%; Score 992.5; DB 14; Length 239;
Best Local Similarity 88.2%; Pred. No. 2.6e-80;
Matches 194; Conservative 10; Mismatches 15; Indels 1; Gaps

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20 Qy 61 SGVPRDRSGSVSGDFTLRIISRVAEADVGVYYCQGLQSGPFTFPGCTKVDIKRGTTVAAPS 120
21 Db 81 SGVPRDRSGSGSGDFTLKIRISRVAEADVGVYYCSQSTHVPPAFGGGTKEIKR-TVAAPS 138
22 Qy 121 VFIPPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYTS 180
23 Db 140 VFIPPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYTS 198
24 Qy 181 LSSLTLSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 220
25 Db 200 LSSLTLSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11
US-09-046-351-82
; Sequence 82, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru

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; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-82

Query Match 86.6%; Score 992.5; DB 14; Length 239;
Best Local Similarity 88.2%; Pred. No. 2.6e-80;
Matches 194; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPLVTPPEPASISCRSSQSLHNSGYIYLDWYLQKFCQSPQLLIYSGSHRA 60
Db 21 DVVMTQSPISLPLVTLGPASISCRSSKSLVHNGNTYILHWYLQKFCQSPRLIYKVSNR 80
QY 61 SGVPDFRFSVSGTDTFLIRISVEAEDGVGYCMOGLQSPFTFGPCTKYDIKRGTVAAAPS 120
Db 81 SGVPDFRFSVSGTDTFLIRISVEAEDGVGYCSQSTHVPPAFGGGTVKVEIKR-TVAAPS 139
QY 121 VFIPTPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSY 180
Db 140 VFIPTPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSY 199
QY 181 LSTLTLSKADYEKKVYACEVTHQGLSPVTKSFNRGEC 220
Db 200 LSTLTLSKADYEKKVYACEVTHQGLSPVTKSFNRGEC 239

RESULT 12
US-09-383-916-6
; Sequence 6, Application US/09383916
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131

```

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Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEODSKDSTYS 199
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Qy 181 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
|||||

Db 200 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 239
|||||

RESULT 14
US-09-046-351-80
; Sequence 80, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-80

Query Match 86.3%; Score 988.5; DB 14; Length 239;
Best Local Similarity 87.7%; Pred. No. 5.9e-80;
Matches 193; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EIVLTQPSLSPVTGPEPASISCRSSQSLHLSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
:::||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 21 DVVMTQPSLSPVTLGQPASISCRSSKSLVHSGNGTYLHWYLRKPGQSPKLLIYKVSNR 80
|||||

Qy 61 SGVPRFSGSVSGTDFTLIRSRVEADGVVYCMOGLSGSTFFGDTKVDIKRGTVAAAPS 120
|||||

Db 81 SGVPRFSGSGSGTDFTLIRSRVEADGVVYFCSGSTHVPFAFGQGTKEIKR-TVAAPS 139
|||||

Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEODSKDSTYS 180
|||||

Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEODSKDSTYS 199
|||||

Qy 181 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 220
|||||

Db 200 LSSTLTLSKADYEHKKVYACEVTHQGLSSPVTKSFNRGEC 239
|||||

RESULT 15
US-09-046-351-84
; Sequence 84, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 ; Search time 29,1837 seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPFLPVTGPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA.New.\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US05\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	1050.5	91.7	239	5	US-09-992-600A-8
2	1015.5	88.6	238	6	US-10-031-355-2
3	1015.5	88.6	238	6	US-10-031-355-11
4	1015.5	88.6	238	6	US-10-031-355-13
5	1015.5	88.6	238	6	US-10-031-355-15
6	1009.5	88.1	219	1	PCT-US02-11854A-11
7	1009.5	88.1	238	1	PCT-US02-11854A-19
8	992.5	86.6	239	5	US-09-758-173-6
9	992.5	86.6	239	5	US-09-326-098-6
10	992.5	86.6	239	5	US-09-948-429B-6
11	992.5	86.6	239	5	US-09-971-631-6
12	992.5	86.6	239	6	US-10-124-807-6
13	992.5	86.6	239	6	US-10-124-805-6
14	992.5	86.6	239	6	US-10-030-390-6
15	987.5	86.2	219	1	PCT-US02-21323-11
16	987.5	86.2	219	1	PCT-US02-21324-11
17	987.5	86.2	219	1	PCT-US02-26321-11
18	986.5	86.1	238	4	US-08-721-612D-19
19	986.5	86.1	238	4	US-08-721-612E-19
20	983.5	85.8	219	5	US-09-791-537-129754
21	976.5	85.2	262	6	US-10-206-008-658
22	971	84.7	228	5	US-09-909-567B-50
23	966.5	84.3	244	6	US-10-206-008-641
24	963.5	84.1	217	5	US-09-791-537-116780
25	963.5	84.1	217	5	US-09-791-537-116791
26	963.5	84.1	241	5	US-09-831-805A-15

27	961.5	83.9	219	1	PCT-US02-11853-11	Sequence 11, Appl
28	961.5	83.9	239	1	PCT-US02-11853-19	Sequence 19, Appl
29	914	79.8	234	6	US-10-153-382-15	Sequence 15, Appl
30	905.5	79.0	235	6	US-10-153-382-7	Sequence 7, Appl
31	903	78.8	238	6	US-10-216-484-107	Sequence 107, Appl
32	902.5	78.8	233	6	US-10-153-382-11	Sequence 11, Appl
33	901	78.6	240	6	US-10-058-120-10	Sequence 10, Appl
34	899	78.4	240	6	US-10-159-006-36	Sequence 36, Appl
35	898.5	78.4	235	1	PCT-US02-20181-4	Sequence 4, Appl
36	898	78.4	220	5	US-09-791-537-122090	Sequence 122090,
37	898	78.4	240	6	US-10-216-310-8	Sequence 8, Appl
38	895.5	78.1	219	5	US-09-791-537-93645	Sequence 93645, A
39	894	78.0	244	5	US-09-831-805A-17	Sequence 17, Appl
40	893.5	78.0	215	1	PCT-US02-12801-129	Sequence 129, Appl
41	893.5	78.0	215	5	US-09-791-537-5099	Sequence 5099, Ap
42	891	77.7	238	6	US-10-216-484-50	Sequence 50, Appl
43	891	77.7	238	6	US-10-216-484-109	Sequence 109, Appl
44	889	77.6	220	5	US-09-669-971-1	Sequence 1, Appl
45	887.5	77.4	215	1	PCT-US02-12801-118	Sequence 118, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-992-600A-8  
; Sequence 8, Application US/09992600A  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91 US4.DIV  
; CURRENT APPLICATION NUMBER: US/09/992,600A  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-992-600A-8

Query Match 91.7%; Score 1050.5; DB 5; Length 239;  
Best Local Similarity 92.7%; Pred. No. 2.7e-54;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy	1	EIVLTQSPFLPVTGPASISCRSSQSLHNSGTYTLDNVLKQPGOSPOLLYSGSRA	60
Db	21	DIVMTQSPFLPVTGPASISCRSSQSLHNSGTYTLDNVLKQPGOSPOLLYSGSRA	80
Qy	61	SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPKVDIKRGTVAAPS	120
Db	81	SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPKVDIKRGTVAAPS	139
Qy	121	VFIPPPDEQLKSGTASVVCVLLNNFYPRKQVQKVNALQSGNSQSVTEQDSKSTYS	180
Db	140	VFIPPPDEQLKSGTASVVCVLLNNFYPRKQVQKVNALQSGNSQSVTEQDSKSTYS	199

QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 2

US-10-031-355-2

; Sequence 2, Application US/10031355

; GENERAL INFORMATION:

; APPLICANT: Glaxo Group Limited

; APPLICANT: Knick, Vincent C

; APPLICANT: Stimmel, Julie B

; APPLICANT: Thurmond, Linda M

; TITLE OF INVENTION: Antibody combination

; FILE REFERENCE: PU3513

; CURRENT APPLICATION NUMBER: US/10/031,355

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: sequence

US-10-031-355-2

Query Match 88.6%; Score 1015.5; DB 6; Length 238;  
Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEASISCRSSQSLHNSGYTYLDWYLRKPGSQPLLIIYQMSHRA 60  
Db 20 DIVMTQSPSLPVTGPEASISCRSSKNLLHNSGITLYLYWYLRKPGSQPLLIIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMGLOSPTFGPTGKVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFPPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 3

US-10-031-355-11

; Sequence 11, Application US/10031355

; GENERAL INFORMATION:

; APPLICANT: Glaxo Group Limited

; APPLICANT: Knick, Vincent C

; APPLICANT: Stimmel, Julie B

; APPLICANT: Thurmond, Linda M

; TITLE OF INVENTION: Antibody combination

; FILE REFERENCE: PU3513

; CURRENT APPLICATION NUMBER: US/10/031,355

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: sequence

US-10-031-355-11

Query Match 88.6%; Score 1015.5; DB 6; Length 238;

Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPVTGPEASISCRSSQSLHNSGYTYLDWYLRKPGSQPLLIIYQMSHRA 60  
Db 20 DIVMTQSPSLPVTGPEASISCRSSKNLLHNSGITLYLYWYLRKPGSQPLLIIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMGLOSPTFGPTGKVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFPPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 4

US-10-031-355-13

; Sequence 13, Application US/10031355

; GENERAL INFORMATION:

; APPLICANT: Glaxo Group Limited

; APPLICANT: Knick, Vincent C

; APPLICANT: Stimmel, Julie B

; APPLICANT: Thurmond, Linda M

; TITLE OF INVENTION: Antibody combination

; FILE REFERENCE: PU3513

; CURRENT APPLICATION NUMBER: US/10/031,355

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 238

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: sequence

US-10-031-355-13

Query Match 88.6%; Score 1015.5; DB 6; Length 238;  
Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEASISCRSSQSLHNSGYTYLDWYLRKPGSQPLLIIYQMSHRA 60  
Db 20 DIVMTQSPSLPVTGPEASISCRSSKNLLHNSGITLYLYWYLRKPGSQPLLIIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMGLOSPTFGPTGKVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFPPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 5

US-10-031-355-15

; Sequence 15, Application US/10031355

; GENERAL INFORMATION:

; APPLICANT: Glaxo Group Limited

; APPLICANT: Knick, Vincent C

; APPLICANT: Stimmel, Julie B

; APPLICANT: Thurmond, Linda M

; TITLE OF INVENTION: Antibody combination

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; FILE REFERENCE: PU3513
; CURRENT APPLICATION NUMBER: US/10/031,355
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: sequence
US-10-031-355-15

Query Match      88.6%; Score 1015.5; DB 6; Length 238;
Best Local Similarity 90.5%; Pred. No. 3e-52;
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 20 DIVMTQSLPLSVTPGEPASISCRSKNLLHNSGITYLYWYLOKPGQSPQLLIYQMSNLA 79
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 80 SGVPDRFSGSVSGTDFTLKISRVEAEDGVVYCAQNLEIPRTFGGQTKVEIKR-TVAAPS 138
QY 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180
Db 139 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 198
QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220
Db 199 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238

RESULT 6
PCT-US02-11854A-11
; Sequence 11, Application PC/TUS0211854A
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: PCT/US02/11854A
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/287,653
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: humanized antibody
PCT-US02-11854A-11

Query Match      88.1%; Score 1009.5; DB 1; Length 219;
Best Local Similarity 88.6%; Pred. No. 6.2e-52;
Matches 195; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYKVSNR 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVVYCFQGSHPVLTFTGGGQTKVEIKR-TVAAPS 119
QY 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180
Db 120 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 179
QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220
Db 180 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 219
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RESULT 7
PCT-US02-11854A-19
; Sequence 19, Application PC/TUS0211854A
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: PCT/US02/11854A
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/287,653
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 238
; TYPE: PRT
; ORGANISM: humanized antibody
PCT-US02-11854A-19

Query Match      88.1%; Score 1009.5; DB 1; Length 238;
Best Local Similarity 88.6%; Pred. No. 6.7e-52;
Matches 195; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 20 DIVMTQSLPLSVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYKVSNR 79
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 80 SGVPDRFSGSVSGTDFTLKISRVEAEDGVVYCFQGSHPVLTFTGGGQTKVEIKR-TVAAPS 138
QY 121 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180
Db 139 VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 198
QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220
Db 199 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238

RESULT 8
US-09-758-173-6
; Sequence 6, Application US/09758173
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,173
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
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; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-6

Query Match 86.6%; Score 992.5; DB 5; Length 239;
Best Local Similarity 87.7%; Pred. No. 6.6e-51;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPLSLPTGPEPASISCRSSQSLHSHNGYTYLDWYLQKPGSQSPOLLIIYSGSHEA 60
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 21 EYVMTQSPLSLPTGPEPASISCRSSQSLKSHNGDTFFLSWYQQKPGQPPRLIIYKVSNRD 80
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 61 SGVPDRFSGSVSGTDTLTISRVRVEAEDVGYYVCMQGLQSPFTFGPGTKVDIKRGTVAAFS 120
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 81 SGVPDRFSGSGAGTDTLTKISAVEAEDVGYYFCGQGTPTPTFGGKTKVEIKR-TVAAFS 139
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 121 VFIPTSPDEQLKSGTASVVCLLNNFYTPRAKQVQKVDNALQSGNSQESVTEQDSKDSYTS 180
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 140 VFIPTSPDEQLKSGTASVVCLLNNFYTPRAKQVQKVDNALQSGNSQESVTEQDSKDSYTS 199
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 220
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 200 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 239
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

RESULT 10
US-09-948-429B-6
; Sequence 6 Application US/09948429B
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskid, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

MOLECULE TYPE: protein  
US-09-948-429B-6

Query Match 86.6%; Score 992.5; DB 5; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPVTGPEPASISCRSSQSLHNSNGDTFLSWYQKPGQPPRLIIYKYSNRD 80  
QY 61 SGVPDRFSGVSGDTFTLRISRVAEADVGVYVCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db 81 SGVPDRFSGGAGDTFTLKISAVEADVGVYFCGGQTRTPPTFGGKVEIKR-TVAAPS 139  
QY 121 VFIFPPDSQSLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 140 VFIFPPDSQSLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 199  
QY 181 LSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11

US-09-971-631-6  
Sequence 6, Application US/09971631  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/971,631  
FILING DATE: 09-Oct-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/383,916  
FILING DATE: 26-AUG-1999  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 86.6%; Score 992.5; DB 5; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;

Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPVTGPEPASISCRSSQSLHNSNGDTFLSWYQKPGQPPRLIIYKYSNRD 80  
QY 61 SGVPDRFSGVSGDTFTLRISRVAEADVGVYVCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db 81 SGVPDRFSGGAGDTFTLKISAVEADVGVYFCGGQTRTPPTFGGKVEIKR-TVAAPS 139  
QY 121 VFIFPPDSQSLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 140 VFIFPPDSQSLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYTS 199  
QY 181 LSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12

US-10-124-807-6  
Sequence 6, Application US/10124807  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/124,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-124-807-6

Query Match 86.6%; Score 992.5; DB 6; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSNGTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPVTGPEPASISCRSSQSLHNSNGDTFLSWYQKPGQPPRLIIYKYSNRD 80

QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGGKTVDIKRGTVAAAPS 120  
Db 81 SGVPRDFSGAGTDFTLKISAVEADVGVYFCGGGTRPTPTFGGKTVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 13  
US-10-124-905-6  
; Sequence 6, Application US/10124905  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/124,905  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-124-905-6  
Query Match 86.6%; Score 992.5; DB 6; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPTPGEPAISCRSSQSLHNSGYTLDWYLQPKQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPTPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGGKTVDIKRGTVAAAPS 120  
Db 81 SGVPRDFSGAGTDFTLKISAVEADVGVYFCGGGTRPTPTFGGKTVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180

Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 14  
US-10-030-390-6  
; Sequence 6, Application US/10030390  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/030,390  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-030-390-6  
Query Match 86.6%; Score 992.5; DB 6; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPTPGEPAISCRSSQSLHNSGYTLDWYLQPKQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPTPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGVYCMQGLQSPFTFGGKTVDIKRGTVAAAPS 120  
Db 81 SGVPRDFSGAGTDFTLKISAVEADVGVYFCGGGTRPTPTFGGKTVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239



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RESULT 15
PCT-US02-21323-11
; Sequence 11, Application PC/TUS0221323
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta
; FILE REFERENCE: X-15240
; CURRENT APPLICATION NUMBER: PCT/US02/21323
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/313,222
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/383,846
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized antibody
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(219)
; OTHER INFORMATION: humanized 266 antibody preferred light chain
PCT-US02-21323-11

Query Match      86.2%; Score 987.5; DB 1; Length 219;
Best Local Similarity 87.3%; Pred. No. 1.2e-50;
Matches 192; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHSGNYLWDYLOKPGQSPQLLIYSGSHRA 60
Db 1 DVVMTQSPFLSPVTLGQSPASISCRSSQSLIYSDGNAYLHWFLQKPGOSPRLLIYKVNRF 60

QY 61 SGVPRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120
Db 61 SGVPRFSGSGGTDFTLTKISRVEAEDVGYVYCSQSTHVPWTFGGGKVEIKR-TVAAPS 119

QY 121 VFIFPPSDEQLKSGTASVVCVLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 180
Db 120 VFIFPPSDEQLKSGTASVVCVLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS 179

QY 181 LSSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 220
Db 180 LSSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 219

```

Search completed: October 9, 2002, 19:21:23  
Job time : 30.1837 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 11.7857 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146  
Sequence: 1 EIVLTQSLPLVTPGPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893.5	78.0	215	2 JE0242	Ig kappa chain NIG
2	877.5	76.6	215	2 JE0244	Ig kappa chain NIG
3	869.5	75.9	215	2 JE0243	Ig kappa chain NIG
4	847.5	74.0	215	2 A23746	Ig kappa chain V-I
5	823	71.8	216	2 JE0241	Ig kappa chain Am3
6	785.5	68.5	219	2 SE2028	Ig kappa chain - m
7	782.5	68.3	219	2 PC4203	Ig kappa chain (mo
8	777.5	67.8	217	2 S42772	Ig kappa chain - m
9	777.5	67.8	219	2 S16112	Ig kappa chain V r
10	769.5	67.1	219	2 S38865	Ig kappa chain - m
11	750.5	65.5	225	2 JL0029	Ig kappa chain pre
12	725	63.3	240	2 S06084	Ig kappa chain pre
13	690	60.2	220	2 A31790	Ig kappa chain V r
14	677	59.1	218	2 S68241	Ig kappa chain V r
15	671	58.6	218	2 JC5810	monoclonal antibod
16	662	57.8	214	2 S68212	Ig kappa chain (Ma
17	651.5	56.8	197	2 S29593	Ig kappa chain (WM
18	640	55.8	210	2 A56169	Ig kappa chain V r
19	640	55.8	234	2 S14237	Ig kappa chain pre
20	636	55.5	234	2 S01320	Ig kappa chain pre
21	634.5	55.4	225	2 S37484	Ig kappa chain - m
22	627	54.7	230	2 S33161	Ig kappa chain - s
23	621.5	54.2	235	2 S25058	Ig kappa chain - m
24	611.5	53.4	178	2 PT0219	Ig kappa chain V-C
25	587.5	51.3	135	2 S52059	JC-kappa protein -
26	549.5	47.9	121	2 S40371	Ig kappa chain - h
27	548	47.8	106	1 K3HU	Ig kappa chain C r
28	546.5	47.7	135	2 S40342	Ig kappa chain - h
29	535.5	46.7	136	2 S40357	Ig kappa chain V-J

30	528.5	46.1	124	2 S03876	Ig kappa chain V-I
31	528	46.1	112	2 S58207	Ig light chain V r
32	527	46.0	117	1 K2HUCM	Ig kappa chain pre
33	524.5	45.8	125	2 S40356	Ig kappa chain - h
34	524	45.7	132	2 S26882	Ig kappa chain V r
35	523.5	45.7	229	2 A20969	Ig kappa chain pre
36	522	45.5	112	2 S58206	Ig light chain V r
37	513	44.8	99	2 A37927	Ig kappa chain C r
38	507.5	44.3	126	2 S40339	Ig kappa chain - h
39	507	44.2	99	2 S26653	Ig kappa chain C r
40	500	43.6	113	1 K2HUTW	Ig kappa chain V-I
41	494	43.1	131	2 S40372	Ig kappa chain V-J
42	489.5	42.7	238	2 A49633	Ig lambda-like cha
43	478.5	41.8	112	1 K2HUML	Ig kappa chain V-I
44	478	41.7	123	2 S40319	Ig kappa chain V r
45	473.5	41.3	130	2 S40321	Ig kappa chain - h

ALIGNMENTS

RESULT 1  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
R:Accession: JE0242  
Submitted to JIPID, November 1998  
A:Description: Structure relationship of kappatype light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 893.5; DB 2; Length 215;  
Best Local Similarity 81.4%; Pred. No. 2.4e-56;  
Matches 179; Conservative 14; Mismatches 22; Indels 5; Gaps 3;

Qy	1	EIVLTQSLPLVTPGPASISCRSSQLHNSNGYTVLDWYLNKPGQSPOLLISGSHRA	60
Db	1	EIVLTQSGTSLSPGERATLSRASQSV--SN--NYLAWYQQKPGQAPSLIYDASSRA	56
Qy	61	SGVPRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS	120
Db	57	TGIPDRFSGSGTDFLTISGLEPDEFVYVYCCQYDRPPWTFGGTKVEIKR-TVAAPS	115
Qy	121	VFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	180
Db	116	VFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS	175
Qy	181	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	220
Db	176	LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2  
JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
R:Accession: JE0244  
Submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>



C;Species: Mus musculus (house mouse)

100 MCEETIETVDEEVRUNCAVCEATETVETCTCTIVKSENNDEC 210

C;Species: Mus musculus (house mouse)

```

RESULT 10
S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Klipp, B.; Becker, W.; Schlaak, M.
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:CROSS-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 67.1%; Score 769.5; DB 2; Length 219;
Best Local Similarity 67.3%; Pred. No. 1.4e-47;
Matches 148; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

QY 1 EIVLTQSPLESLPVTPGPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHRA 60
DB 1 ELVNTQSPLESLVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSLPKLLIYIVSNRF 60

QY 61 SGVPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 61 ELVNTQSPLESLVSLGDAQASISCRSSQSLVHTNGTYLHWYLOKPGSLPKLLIYIVSNRF 60

QY 61 SGVPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 61 SGVPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180

QY 140 TVSIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 199
DB 140 TVSIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 199

Query Match 63.3%; Score 725; DB 2; Length 240;
Best Local Similarity 63.3%; Pred. No. 2.2e-44;
Matches 140; Conservative 31; Mismatches 48; Indels 2; Gaps 2;

QY 1 EIVLTQSPLESLPVTPGPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHR 59
DB 21 DFVMTQSPSSSLAYSAAGEIVTINCKSSQSLFYSGNKNYLAHWYQKPGQSPKLLIYWASTR 80

QY 60 ASGVDPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
DB 81 QSGVDPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 139

QY 120 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 179
DB 140 TVSIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 199

QY 180 SLSTLTLSKADYERHKHYACEVTHQGLSSPVTKSFNRGEC 220
DB 200 SMSSTLTLSKADYERHNSYTCETHTKTSTSPIVKSFNRNEC 240

RESULT 13
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:CROSS-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 690; DB 2; Length 220;
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QY 61 SGVPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 67 SGVPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 125

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180
DB 126 VSIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 185

QY 181 LSSTLTLSKADYERHKHYACEVTHQGLSSPVTKSFNRGEC 220
DB 186 MSSTLTLSKADYERHNSYTCETHTKTSTSPIVKSFNRNEC 225

RESULT 12
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c
A:Reference number: S06084; MUID:90016888
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:CROSS-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 725; DB 2; Length 240;
Best Local Similarity 63.3%; Pred. No. 2.2e-44;
Matches 140; Conservative 31; Mismatches 48; Indels 2; Gaps 2;

QY 1 EIVLTQSPLESLPVTPGPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHR 59
DB 21 DFVMTQSPSSSLAYSAAGEIVTINCKSSQSLFYSGNKNYLAHWYQKPGQSPKLLIYWASTR 80

QY 60 ASGVDPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 119
DB 81 QSGVDPDRFSGVSGNDFTLIRISVEAEDGVGYCMQGLQSPFTFGPGTKVDIKRGTVAAAP 139

QY 120 SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 179
DB 140 TVSIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTY 199

QY 180 SLSTLTLSKADYERHKHYACEVTHQGLSSPVTKSFNRGEC 220
DB 200 SMSSTLTLSKADYERHNSYTCETHTKTSTSPIVKSFNRNEC 240

RESULT 13
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:CROSS-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 690; DB 2; Length 220;
```







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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:54 ; Search time 6.73469 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 1146  
Sequence: 1 EIVLTQSLPLSVTPGEPAS.....EYTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	548	47.8	106	1	KAC_HUMAN	P01834 homo sapien
2	527	46.0	117	1	KV2E_HUMAN	P06309 homo sapien
3	500	43.6	113	1	KV2D_HUMAN	P01617 homo sapien
4	478.5	41.8	112	1	KV2C_HUMAN	P01616 homo sapien
5	467.5	40.8	115	1	KV2A_HUMAN	P01614 homo sapien
6	455	39.7	113	1	KV2B_HUMAN	P01615 homo sapien
7	444	38.7	133	1	KV2F_HUMAN	P06310 homo sapien
8	432	37.7	113	1	KV2E_MOUSE	P03976 mus musculus
9	429	37.4	113	1	KV2G_MOUSE	P01631 mus musculus
10	423	36.9	113	1	KV2F_MOUSE	P01630 mus musculus
11	402	35.1	112	1	KV2D_MOUSE	P01629 mus musculus
12	394.5	34.4	108	1	KV1_CANFA	P01618 canis famil
13	394	34.4	113	1	KV2C_MOUSE	P01628 mus musculus
14	387	33.8	112	1	KV2A_MOUSE	P01626 mus musculus
15	370	32.3	129	1	KV3L_HUMAN	P18135 homo sapien
16	369	32.2	129	1	KV3M_HUMAN	P18136 homo sapien
17	368.5	32.2	114	1	KV4A_HUMAN	P01623 homo sapien
18	367	32.0	106	1	KACB_RAT	P01835 rattus norv
19	366.5	32.0	134	1	KV4C_HUMAN	P06314 homo sapien
20	366	31.9	109	1	KV3B_HUMAN	P01620 homo sapien
21	366	31.9	109	1	KV3D_HUMAN	P01622 homo sapien
22	362	31.6	120	1	KV2B_MOUSE	P01627 mus musculus
23	359	31.3	106	1	KACA_RAT	P01836 rattus norv
24	357	31.2	109	1	KV3E_HUMAN	P01623 homo sapien
25	357	31.2	109	1	KV3G_HUMAN	P04206 homo sapien
26	354	30.9	133	1	KV4B_HUMAN	P06313 homo sapien
27	351	30.6	108	1	KV3A_HUMAN	P01619 homo sapien
28	350	30.5	106	1	KAC_MOUSE	P01837 mus musculus
29	349.5	30.5	128	1	KV3K_HUMAN	P06311 homo sapien
30	343.5	30.0	111	1	KV3M_MOUSE	P01665 mus musculus
31	340.5	29.7	111	1	KV3L_MOUSE	P01664 mus musculus
32	340	29.7	109	1	KV3F_HUMAN	P01624 homo sapien
33	338.5	29.5	111	1	KV3O_MOUSE	P01667 mus musculus

ALIGNMENTS

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hieber P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROV).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(in) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."			

P01673 mus musculus  
P04207 homo sapien  
P01671 mus musculus  
P01666 mus musculus  
P01670 mus musculus  
P01660 mus musculus  
P01668 mus musculus  
P01669 mus musculus  
P01662 mus musculus  
P01672 mus musculus  
P01656 mus musculus  
P01661 mus musculus

34 338.5 29.5 111 1 KV3U\_MOUSE  
35 338 29.5 129 1 KV3H\_HUMAN  
36 336.5 29.4 111 1 KV3S\_MOUSE  
37 335.5 29.3 111 1 KV3N\_MOUSE  
38 334.5 29.2 111 1 KV3R\_MOUSE  
39 333.5 29.1 111 1 KV3H\_MOUSE  
40 332 29.0 110 1 KV3P\_MOUSE  
41 331.5 28.9 111 1 KV3O\_MOUSE  
42 326.5 28.5 111 1 KV3J\_MOUSE  
43 326.5 28.5 111 1 KV3T\_MOUSE  
44 324.5 28.3 111 1 KV3C\_MOUSE  
45 324.5 28.3 131 1 KV3I\_MOUSE

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RX SEQUENCE (BENCE-JONES PROTEIN AG).
RP MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RX SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RP MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC -----
CC EMBL; J00241; AAA5989.1; -.
CC EMBL; V00557; CAA23823.1; -.
CC PIR; A02116; K3HU.
CC HSSP; P01842; 7FAB.
CC MIN; 147200; -.
CC InterPro; IPR003006; Iq_MHC.
CC InterPro; IPR003597; Iq_C1.
CC Pfam; PF00047; Iq; 1.
CC SMART; SM00407; IGCL; 1.
CC PROSITE; PS00290; Iq_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region.
CC NON_TER 1 1
CC DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
CC VARIANT 106 106 V -> L (IN INV(1,2) MARKER).
CC /FTID=VAR_003897.
CC CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
CC CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
CC SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
Query Match 47.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.2e-40; Mismatches 0; Indels 0; Gaps 0;
Matches 106; Conservative 0;
QY 115 TVAAPSVFFPPSDRLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 1 TVAAPSVFFPPSDRLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 175 KDSYSLSLTSLTKADYKKHKVYACEVTHOGLSSPVTKSNRGEK 220
Db 61 KDSYSLSLTSLTKADYKKHKVYACEVTHOGLSSPVTKSNRGEK 106
RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
ID KV2E_HUMAN
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity."
RL Nature 309:73-76(1984).
CC -----
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CC -----
CC EMBL; Z00009; -. NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
CC InterPro; IPR003006; Iq_MHC.
CC InterPro; IPR003596; Iq_V.
CC Pfam; PF00047; Iq; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC NON_TER 1 1
CC SIGNAL <1 4
CC CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
CC DOMAIN 28 43 FRAMEWORK-1.
CC DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 59 65 FRAMEWORK-2.
CC DOMAIN 66 97 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 98 106 FRAMEWORK-3.
CC DOMAIN 107 116 COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 117 117 FRAMEWORK-4.
CC DISULFID 27 97 BY SIMILARITY.
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Query Match 46.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 2.9e-38; Mismatches 6; Indels 0; Gaps 0;
Matches 101; Conservative 6;
QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKQSPQLIYSGSHRA 60
Db 5 DIVMTQSPISLPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKQSPQLIYLSNRA 64
QY 61 SGVPDRFSGSVSGTDTLRLISRVEAEADVGVYICMQLQSPFTFGPGTKVDIAR 113
Db 65 SGVPDRFSGSVSGTDTLRLISRVEAEADVGVYICMQLQSPFTFGPGTKVKEIKR 117
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glennier G.G.;
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RT RT Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR: A01888; K2HUTW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 43.6%; Score 500; DB 1; Length 113;
Best Local Similarity 82.3%; Pred. No. 5.5e-36;
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYSGSRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYLSNRA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
type)".
RL Hope-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation."
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.8%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 3.2e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYSGSRA 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVDPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVDPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 41.8%; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.8%; Pred. No. 3.6e-34;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYSGSRA 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYLSNRA 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 SGVPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
KV2A_HUMAN STANDARD; PRT; 115 AA.
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
type)".
RL Hope-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation."
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.8%; Score 467.5; DB 1; Length 115;
Best Local Similarity 79.8%; Pred. No. 3.2e-33;
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYSGSRA 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIVMTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPQLLIYLSYR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 ASGVDPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 ASGVDPDRFSGSVSGTDFTLIRSRVEADGVVYCMQGLQSPFTFGPGTKVDIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
KV2B_HUMAN STANDARD; PRT; 113 AA.
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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	Ig kappa chain V-II region FR.
DE	Homo sapiens (Human).
DJ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;	
[1]	
SEQUENCE.	
PUBMEDLINE=76253627; PubMed=821524;	
Riesen W.F., Jaton J.-C.;	"Variable region sequence of the light chain from a Waldenstrom's IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).	
-1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.	
PIR: A01886; K2HUFR.	
InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam: PF00047; Ig_1. SMART: SM00406; IGv_1. Immunoglobulin v region.	
DOMAIN 1 23 FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4. BY SIMILARITY.	
DISULFID 23 113 NON_TER 113 SEQUENCE 113 AA; L2660 MW; OCODA39E46DB96BE CRC64;  Query Match 39.7%; Score 455; DB 1; Length 113; Best Local Similarity 74.3%; Pred. No. 3.7e-32; Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;	
QY 1 EIVLTQSPLSLVPTGPPEASISCRSSQLLSHNGYYILDWYLKPKQCSPQLLIYSCSHRA 60 ::                    : ::                                   Db 1 DVVTQTSPFLVLTPGERASIICRSSQSIIIRBGTIILEWLKYLOKPQGSELLIYUSSRD 60                     :                                   QY 61 SGVPDRFGSGSVGGTDFTLRIARSVEADVGVIYCQMGLSQPFPGTKVDIKR 113                     :                                   Db 61 SGVPDRFGSDGSCTDFTLKTRVQAEDVGVIYCMQATZSPYTFGGQTKLZIKR 113                     :	
RESULT 7	
ID KV2F_HUMAN STANDARD; PRT: 133 AA.	
AC OPe310:	
Dt 01-JAN-1988 (Rel. 06, Created)	
Tl 01-JAN-1988 (Rel. 06, Last sequence update)	
De 15-JUL-1999 (Rel. 38, Last annotation update)	
DT DE Ig kappa chain V-II region RPMI 6410 precursor.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_Taxid=9606;	
[1]	
SEQUENCE FROM N.A.	
PUBMEDLINE=86041852; Pubmed=2997711;	
Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;	"Human immunoglobulin kappa light chain genes of subgroups II and III.";
Nucleic Acids Res. 13:6499-6513(1985). ----- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensel@isb-sib.ch). ----- EMBL: Z00020; CAA77315.1; --	

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE
RX	MEDLINE=83256427; PubMed=6409088;
RA	Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT	"A new isotype sequence (V kappa 27) of the variable region of kappa
RT	light chains from a mouse hybridoma-derived anti-(streptococcal group
RT	A polysaccharide) antibody containing an additional cysteine residue
RT	Application of the dimethylaminoazobenzene isothiocyanate technique
RT	for the isolation of peptides.;"
RL	Biochem. J. 211:173-180(1983).
CC	-1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC	ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC	
DR	PIR; A01913; KVM57S.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
KW	Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT	DOMAIN 1 23
FT	FT DOMAIN 24 39
FT	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 40 54
FT	FT DOMAIN 55 61
FT	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 62 93
FT	FT DOMAIN 94 102
FT	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 103 112
FT	FT DISULFID 23 93
FT	FT NON_TER 113 113
FT	FT
SO	SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;
Query Match 36.9%; Score 423; DB 1; Length 113;	
Best Local Similarity 74.3%; Pred. No. 1.9e-29;	
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps	
Qy	1 EIVLTQSPILSPVTPCEPASISCRSSQSLHSNGYITLDWYLOKQPSQLLIYSGSHRA 60
Db	1 DIVMTQTAPSAVLTGCVSYISCRSSKLSLHSGNTLYWFLQPGCPLLIIYRMSNLA 60
Qy	61 SGVPDFSGSGVSDPTFLIRSRVAEADVGVYCMQGLSPFTGPGTKVDIKR 113
Db	61 SGVPDFSGSGSGTFTFLIRSRVAEADVGVYCMQREYPTFGGKTLEIKR 113
RESULT 11	
KV2D_MOUSE	ID KV2D_MOUSE STANDARD; PRT; 112 AA.
AC	P01629;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-II region 2S1.3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE
RX	MEDLINE=83055101; PubMed=7141411;
RA	Herbst H., Chang J.-Y., Abersold R., Braun D.G.;
RT	"Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
RT	the group A streptococcal polysaccharide.;"
RT	Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC	-1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC	ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC	
DR	PIR; A01911; KVMSS1.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
KW	Immunoglobulin V region; Monoclonal antibody
FT	DOMAIN 1 23
FT	FT DOMAIN 24 39
FT	COMPLEMENTARITY-DETERMINING-1.





